

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:22:13 ; Search time 186 Seconds  
(without alignments)  
18.898 Million cell updates/sec

Title: US-10-807-553-2

Perfect score: 48

Sequence: 1 HDAPIGYD 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

1: A\_Geneseq\_21: \*  
2: Geneseqp1980s: \*  
3: Geneseqp1990s: \*  
4: Geneseqp2000s: \*  
5: Geneseqp2001s: \*  
6: Geneseqp2002s: \*  
7: Geneseqp2003as: \*  
8: Geneseqp2004s: \*  
9: Geneseqp2005s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	8	2	AAW54884 Isozyme-8
2	48	100.0	8	6	ABB99501 Amino aci
3	48	100.0	8	6	ABG76120 Pslepa110
4	48	100.0	8	9	AEA89881 Receptor
5	48	100.0	30	9	AEA89971 Receptor
6	48	100.0	737	5	AAO18490 Human ins
7	48	100.0	737	6	ADA50073 Mouse pro
8	48	100.0	737	6	AAE39167 Mouse pro
9	48	100.0	737	7	ADE57469 Human pro
10	48	100.0	737	7	ADE57451 Human pro
11	48	100.0	737	7	ADE58354 Human pro
12	48	100.0	737	7	ADE57531 Rat prote
13	48	100.0	737	7	ADE57533 Human pro
14	48	100.0	737	7	ADE58352 Rat prote
15	48	100.0	737	7	ADE57535 Rat prote
16	48	100.0	737	7	ADE57537 Rat prote
17	48	100.0	737	7	ADE57539 Rat prote
18	48	100.0	737	7	ADE57527 Rat prote
19	48	100.0	737	7	ADE57529 Human pro
20	48	100.0	737	9	ADY80150 Amino aci
21	48	100.0	737	9	ADY80138 Amino aci
22	48	100.0	737	9	ADY80140 Amino aci
23	48	100.0	737	9	ADY80151 Amino aci
24	44	91.7	8	6	ABB99506 Amino aci

25	44	91.7	8	6	ABB99512 Amino aci
26	44	91.7	8	6	ABG76125 Pslepa110
27	44	91.7	8	6	ABG76131 Pslepa110
28	44	91.7	8	9	AEA89893 Receptor
29	44	91.7	8	9	AEA89887 Receptor
30	44	91.7	8	9	AEA89909 Receptor
31	43	89.6	8	2	AAW54889 Isozyme-8
32	43	89.6	8	2	AAW54892 Isozyme-8
33	43	89.6	8	6	ABB99507 Amino aci
34	43	89.6	8	6	ABG76126 Pslepa110
35	43	89.6	8	9	AEA89933 Receptor
36	43	89.6	8	9	AEA89888 Receptor
37	42	87.5	8	2	AAW54894 Isozyme-8
38	42	87.5	8	2	AAW54895 Isozyme-8
39	42	87.5	8	6	ABB99508 Amino aci
40	42	87.5	8	6	ABG76127 Pslepa110
41	42	87.5	8	9	AEA89907 Receptor
42	42	87.5	8	9	AEA89889 Receptor
43	42	87.5	11	2	AAW17460 Protein k
44	42	87.5	11	2	ADY80144 Peptide a
45	40	83.3	8	2	AAW54890 Isozyme-8
46	40	83.3	8	2	AAW54891 Isozyme-8
47	40	83.3	8	2	AAW54887 Isozyme-8
48	40	83.3	8	2	AAW54888 Isozyme-8
49	40	83.3	8	6	ABB99511 Amino aci
50	40	83.3	8	6	ABB99513 Amino aci
51	40	83.3	8	6	ABG76130 Pslepa110
52	40	83.3	8	6	ABG76132 Pslepa110
53	40	83.3	8	9	AEA89892 Receptor
54	40	83.3	8	9	AEA89897 Receptor
55	40	83.3	8	9	AEA89894 Receptor
56	40	83.3	8	9	AEA89899 Receptor
57	39	81.2	8	2	AAW54893 Isozyme-8
58	38	79.2	8	2	AAW54898 Isozyme-8
59	38	79.2	8	9	AEA89884 Receptor
60	38	79.2	18	9	AEA89974 Receptor
61	38	79.2	35	6	ABR98412 Tumour ce
62	38	79.2	35	7	ADC84758 MCF-7 bre
63	38	79.2	682	5	AAO18491 Human ins
64	38	79.2	682	8	ADM41441 Human pro
65	38	79.2	683	7	ADC37371 Nucleat f
66	38	79.2	683	8	ADJ96615 Human pro
67	38	79.2	683	8	ADM41445 Human pro
68	38	79.2	683	8	ADM41451 Human pro
69	38	79.2	683	8	ADQ96474 T cell ac
70	38	79.2	683	8	ADQ97369 Human can
71	38	79.2	683	9	ADY15668 PRO poly
72	38	79.2	683	9	AEC01607 Human pro
73	38	79.2	702	8	ADO97364 Mouse can
74	38	79.2	715	8	ADM41450 His-tagge
75	38	79.2	918	8	ADM41449 Glutathio
76	37.5	78.1	14	2	AAW54901 Isozyme-8
77	37	77.1	8	9	AEA89945 Receptor
78	37	77.1	2203	9	AEA89945 Receptor
79	37	77.1	2203	7	ADD46697 Rat prote
80	37	77.1	2203	7	ADD46697 Rat prote
81	36	75.0	8	6	ABB99516 Amino aci
82	36	75.0	8	6	ABB99505 Amino aci
83	36	75.0	8	6	ABG76135 Pslepa110
84	36	75.0	8	6	ABG76124 Pslepa110
85	36	75.0	8	9	AEA89897 Receptor
86	36	75.0	8	9	AEA89886 Receptor
87	36	75.0	8	9	AEA89944 Receptor
88	36	75.0	8	2	AAW54886 Isozyme-8
89	35	72.9	6	9	AEA89898 Receptor
90	35	72.9	8	2	AAW54885 Isozyme-8
91	35	72.9	8	6	ABB99509 Amino aci
92	35	72.9	8	6	ABB99510 Amino aci
93	35	72.9	8	6	ABG76129 Pslepa110
94	35	72.9	8	6	ABG76128 Pslepa110
95	35	72.9	8	9	AEA89890 Receptor
96	35	72.9	8	9	AEA89910 Receptor
97	35	72.9	8	9	AEA89935 Receptor

98	35	72.9	8	9	AEA89891
99	35	72.9	8	9	AEA89934
100	35	72.9	8	9	AEA89929

## ALIGNMENTS

## RESULT 1

AAW54884 standard; peptide; 8 AA.

AAW54884;

24-SEP-1998 (first entry)

Isozyme-specific agonist peptide epsilon VI-7;E7.

epithelial protein kinase C; ischaemic injury; hypoxic exposure.

Synthetic.

MO981729-A1.

30-APR-1998.

18-OCT-1997 97WO-US018716.

18-OCT-1996; 96US-0028724P.

(STRD ) UNIV LELAND STANFORD JUNIOR.

Mochly-Rosen D;

WPI; 1998-261181/23.

Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions.

Claim 1; Page 32; 47pp; English.

The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections

Sequence 8 AA;

Query Match 100.0%; Score 48; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HDAPIGYD 8

1 HDAPIGYD 8

AB899501 standard; peptide; 8 AA.

AB899501;

03-MAR-2003 (first entry)

Amino acid sequence of a pseudo-epsilon RACK peptide.

Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;

protein kinase C; PKC; tissue damage; ischaemia; hypoxia.

Synthetic.

XX MO200278600-A2.

XX 10-OCT-2002

XX 09-NOV-2001; 2001WO-US051600.

XX 10-NOV-2000; 2000US-0247830P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 2003-092868/08.

XX New composition comprising pseudo-epsilonRACK peptides, useful for treating tissue damage due to ischemia or hypoxia.

XX Claim 6; Page 27; 30pp; English.

XX The present sequence represents a pseudo-epsilon RACK octapeptide. RACKs

XX (receptors for activated C-kinase) are anchoring molecules, which

XX selectively anchor activated protein kinase C (PKC) isozymes to their

XX respective subcellular sites. Compositions comprising pseudo-epsilon RACK

XX peptides are useful for reducing injury to a cell or tissue exposed to an

XX ischaemic or hypoxic condition. The composition is useful for treating

XX tissue damage due to ischaemia or hypoxia

XX Sequence 8 AA;

Query Match 100.0%; Score 48; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HDAPIGYD 8

1 HDAPIGYD 8

ABG76120 standard; peptide; 8 AA.

ABG76120;

07-MAY-2003 (first entry)

Psepsilon RACK peptide.

Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;

KW receptor for activated C-kinase; myocardial infarction;

KW cardiac ischaemia; psepsilon RACK.

OS Synthetic.

US2002168354-A1.

14-NOV-2002.

09-NOV-2001; 2001US-00007363.

10-NOV-2000; 2000US-0247830P.

(MOCH/) MOCHLY-ROSEN D.

Mochly-Rosen D;

WPI; 2003-092868/08.

New composition comprising pseudo-epsilonRACK peptides, useful for treating tissue damage due to ischemia or hypoxia.

Claim 7; Page 8; 17pp; English.

XX The invention relates to reducing injury to a cell or tissue exposed to  
CC an ischaemic or hypoxic condition, comprising administering to the cell  
CC or tissue a pepsinogen Receptor for Activated C-Kinase (RACK) peptide.  
CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).  
CC The method is useful in treating or protecting cells and tissues from  
CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia  
CC or myocardial infarction. The present sequence is the pepsinogen RACK  
CC peptide of the invention  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 48; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8  
RESULT 4  
AEA89881  
ID AEA89881 standard; peptide, 8 AA.  
AC AEA89881;  
XX 08-SEP-2005 (first entry)  
XX Receptor for activated C kinase (RACK) peptide #3.  
XX  
XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;  
KM fibrosis; pulmonary fibrosis; septic shock; ischemia;  
KM inflammatory bowel disease; autoimmune disease; multiple sclerosis;  
KM Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;  
KM diabetes mellitus; pulmonary disease;  
KM chronic obstructive pulmonary disease; asthma;  
KM receptor for activated C kinase; RACK; antiinflammatory; dermatological;  
KM hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;  
KM antidiabetic; CNS-gen.; antithyroid; antiarthritic; antipneumatic;  
KM vasotropic; cardiant.  
OS Homo sapiens.  
XX  
XX WO2005059124-A2.  
XX 30-JUN-2005.  
XX 13-DEC-2004; 2004WO-US041854.  
XX 11-DEC-2003; 2003US-0529223P.  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX Mochly-Rosen D, Chen LE;  
XX WPI; 2005-479333/48.  
XX  
XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist  
XX peptide useful for treating fibrotic or inflammatory disease, involves  
XX substituting charged amino acid in agonist peptide with another uncharged  
XX amino acid.  
XX  
XX Claim 6; SEQ ID NO 3; 90pp; English.  
XX  
XX The invention relates to a method of converting a protein kinase C (PKC)  
XX agonist peptide or peptidomimetic to a PKC antagonist peptide or  
XX peptidomimetic, involving substituting at least one amino acid in the  
XX agonist peptide or peptidomimetic with an amino acid that converts the  
XX PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or  
XX peptidomimetic. The invention also relates to a method of inhibiting the  
XX activity of a protein kinase C (PKC) enzyme, involving contacting the

CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide  
CC derived from a PKC agonist peptide or peptidomimetic where at least one  
CC amino acid in the agonist peptide or peptidomimetic is substituted with  
CC another amino acid sufficient to convert the peptide or peptidomimetic  
CC into an antagonist peptide or peptidomimetic. The method is useful for  
CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist  
CC peptide or peptidomimetic. The antagonist peptide is useful for treating  
CC a disease or condition modulated by epsilon-PKC such as scleroderma,  
CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory  
CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre  
CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes  
CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease  
CC and asthma. This sequence represents a receptor for activated C kinase  
CC (RACK) peptide used in the method of the invention.  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 48; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8  
RESULT 5  
AEA89971  
ID AEA89971 standard; peptide, 30 AA.  
AC AEA89971;  
XX 08-SEP-2005 (first entry)  
XX Receptor for activated C kinase (RACK) peptide #9.  
XX  
XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;  
KM fibrosis; pulmonary fibrosis; septic shock; ischemia;  
KM inflammatory bowel disease; autoimmune disease; multiple sclerosis;  
KM Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;  
KM diabetes mellitus; pulmonary disease;  
KM chronic obstructive pulmonary disease; asthma;  
KM receptor for activated C kinase; RACK; antiinflammatory; dermatological;  
KM hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;  
KM antidiabetic; CNS-gen.; antithyroid; antiarthritic; antipneumatic;  
KM vasotropic; cardiant.  
OS Homo sapiens.  
XX  
XX WO2005059124-A2.  
XX 30-JUN-2005.  
XX 13-DEC-2004; 2004WO-US041854.  
XX 11-DEC-2003; 2003US-0529223P.  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX Mochly-Rosen D, Chen LE;  
XX WPI; 2005-479333/48.  
XX  
XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist  
XX peptide useful for treating fibrotic or inflammatory disease, involves  
XX substituting charged amino acid in agonist peptide with another uncharged  
XX amino acid.  
XX  
XX Disclosure; SEQ ID NO 93; 90pp; English.  
XX  
XX The invention relates to a method of converting a protein kinase C (PKC)  
XX agonist peptide or peptidomimetic to a PKC antagonist peptide or

CC peptidomimetic, involving substituting at least one amino acid in the  
CC agonist peptide or peptidomimetic with an amino acid that converts the  
CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or  
CC peptidomimetic. The invention also relates to a method of inhibiting the  
CC activity of a protein kinase C (PKC) enzyme, involving contacting the  
CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide  
CC derived from a PKC agonist peptide or peptidomimetic where at least one  
CC amino acid in the agonist peptide or peptidomimetic is substituted with  
CC another amino acid sufficient to convert the peptide or peptidomimetic  
CC into an antagonist peptide or peptidomimetic. The method is useful for  
CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist  
CC peptide or peptidomimetic. The antagonist peptide is useful for treating  
CC a disease or condition modulated by epsilon-PKC such as scleroderma,  
CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory  
CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre  
CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes  
CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease  
CC and asthma. This sequence represents a receptor for activated C kinase  
CC (RACK) peptide used in the method of the invention.

XX  
XX Sequence 30 AA;

Query Match 100.0%; Score 48; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.056; Mismatches 0; Gaps 0;  
Matches 8; Conservative 0; Indels 0;

Qy 1 HDAPIGYD 8  
|||  
DB 15 HDAPIGYD 22

RESULT 6  
AA018490  
ID AA018490 standard; protein; 737 AA.

AC AA018490;

XX 11-OCT-2002 (first entry)

XX Human insulin receptor signaling modifier SEQ ID NO: 2.

DE Human insulin receptor signaling; insulin receptor signaling modifier;

KW Human; insulin receptor signaling; insulin receptor signaling modifier;

XX ISM; diabetes; metabolic syndrome; antidiabetic.

OS Homo sapiens.

XX MO200255664-AA2.

XX 18-JUL-2002.

PF 11-JAN-2002; 2002WO-US001048.

XX 12-JAN-2001; 2001US-0261226P.

XX 12-JAN-2001; 2001US-0261303P.

XX 12-JAN-2001; 2001US-0261304P.

XX 12-JAN-2001; 2001US-0261335P.

XX 12-JAN-2001; 2001US-0261361P.

XX 12-JAN-2001; 2001US-0261457P.

XX 12-JAN-2001; 2001US-0261458P.

XX 12-JAN-2001; 2001US-0261459P.

XX 12-JAN-2001; 2001US-0261518P.

XX 12-JAN-2001; 2001US-0261531P.

XX 12-JAN-2001; 2001US-0261589P.

XX 12-JAN-2001; 2001US-0261590P.

XX 12-JAN-2001; 2001US-0261694P.

XX 12-JAN-2001; 2001US-0261695P.

XX 12-JAN-2001; 2001US-0261697P.

EXBLIXIS INC.

XX Seidel-Dugan C, Ferguson KC, Kidd T;  
PI WPI; 2002-599664/64.  
DR N-PSDB; AAL48609.

XX Identifying an insulin receptor signaling modulator, useful as drug  
PT targets for treating diabetes or metabolic disorders, comprises  
PT contacting an assay system comprising insulin receptor signaling  
PT modifiers with a test agent.

PS Disclosure; Page 32-35; 232pp; English.

XX The present invention relates to a method of identifying a candidate  
CC insulin receptor (INR) signaling modulating agent, involving contacting  
CC an assay system comprising an insulin receptor signaling modifier (ISM)  
CC polypeptide or nucleic acid with a test agent, and detecting a test agent  
CC biased activity of the assay system. The method is useful for  
CC identifying candidate INR signaling modulating agents. ISM genes may be  
CC used as drug targets for treatment of disorders related to INR signaling  
CC such as diabetes or metabolic syndrome. ISM nucleic acids and  
CC polypeptides are useful for identifying and testing agents that modulate  
CC ISM function and for other applications related to the involvement of ISM  
CC in INR signaling, and for identifying subjects having a predisposition to  
CC such diseases associated with INR signaling. The present sequence is an  
CC ISM protein described in the exemplification of the invention

XX Sequence 737 AA;

Query Match 100.0%; Score 48; DB 5; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Gaps 0;  
Matches 8; Conservative 0; Indels 0;

Qy 1 HDAPIGYD 8  
|||  
DB 85 HDAPIGYD 92

RESULT 7  
ADA50073  
ID ADA50073 standard; protein; 737 AA.

AC ADA50073;

XX 20-NOV-2003 (first entry)

DE Mouse protein kinase C protein related to mouse skin cancer models.

XX UV radiation; human skin; non-human animal skin; FVB/N mouse;

XX human cancer; epithelial tissue; non-melanoma skin cancer; NMSC;

XX squamous cell carcinoma; SSC; animal model system; transgenic animal;

XX cancer development; cancer progression; cancer treatment;

XX protein kinase C; PKC; mouse epidermis; cyclostatic; vulnary;

XX dermatological; cell therapy; photodamage; photocaging; skin wounding;

XX PKC transgene; mouse; T7 tag; enzyme; protein kinase C epsilon.

OS Chimeric.

XX Mus musculus.

XX Enterobacteria phage T7.

XX US2003051258-A1.

XX 13-MAR-2003.

XX 27-AUG-2002; 2002US-00228931.

XX 30-JAN-2001; 2001US-00772647.

XX (VERM/) VERMA A K.

XX (WHEB/) WHEELER D L.

XX Verma AK, Wheeler DL;

DR WPI; 2003-596530/56.  
 DR N-PSDB; ADA50078.  
 PT Identifying an agent for reducing or preventing an effect of UV radiation  
 PT on animal skin for treating or preventing e.g., squamous cell carcinoma  
 PT by exposing an FVB/N mouse and administering at least one agent.  
 PS Disclosure; Page 14-16; 18pp; English.  
 XX  
 CC This invention relates to a novel method for the identification of an  
 CC agent for reducing or preventing an effect of UV radiation on skin of a  
 CC human or non-human animal. The preferred method of the invention  
 CC comprises exposing an FVB/N mouse to UV radiation and administering at  
 CC least one agent. A majority of human cancers originate from epithelial  
 CC tissue, for example non-melanoma skin cancer (NMSC) and squamous cell  
 CC carcinoma (SCC). As such, there is a need for a good animal model system  
 CC for studying how these cancers develop, progress and can be treated. The  
 CC present invention provides an FVB/N mouse that expresses more protein  
 CC kinase C (PKC) in its epidermis than that of a wild-type mouse which may  
 CC be a useful model for development and treatment of skin cancer,  
 CC particularly SCC, in human and non-human mammalian animals. The invention  
 CC may provide a method for the development of compounds with cytostatic,  
 CC veterinary or dermatological activity through use in cell therapy. The  
 CC method may therefore prove useful for preparing a composition for treating  
 CC or preventing SCC, photocarcinoma, photocaging or skin wounding induced by UV  
 CC radiation. The present sequence is that of mouse protein kinase C (PKC)  
 CC with a 5' T7 tag, the coding DNA sequence of which was used in the  
 CC production of a PKC transgene during the exemplification of the  
 CC invention.  
 CC  
 CC Sequence 737 AA;  
 SQ  
 Query Match 100.0%; Score 48; DB 6; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HDAPIGYD 8  
 Db 85 HDAPIGYD 92  
 RESULT 8  
 AAE39167  
 ID AAE39167 standard; protein; 737 AA.  
 XX  
 AC AAE39167;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Mouse protein kinase C-epsilon -T7 tag chimeric protein.  
 XX  
 KW Mouse; protein kinase C-epsilon; PKC-epsilon; squamous cell carcinoma;  
 KW SCC; skin cancer; enzyme; chimeric; fusion protein.  
 XX  
 OS Chimeric- Mus musculus.  
 OS Chimeric- Bacteriophage T7.  
 XX  
 PN US6521815-B1.  
 XX  
 PD 18-FEB-2003.  
 XX  
 PF 30-JAN-2001; 2001US-00772647.  
 XX  
 PR 30-JAN-2001; 2001US-00772647.  
 XX  
 PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
 XX  
 PI Verma AK, Reddig PJ, Jansen AP;  
 XX  
 DR WPI; 2003-352430/33.  
 DR N-PSDB; AAD59551.  
 XX  
 PT Novel genetically modified FVB/N mouse having epidermal cells that

PT comprise a protein kinase C-epsilon activity higher than that of wild-  
 PT type FVB/N epidermal cells, for investigating development of metastatic  
 PT disease.  
 XX  
 PS Disclosure; Col 23-28; 16pp; English.  
 XX  
 CC The present invention provides novel genetically modified FVB/N mouse  
 CC having epidermal cells that comprise a protein kinase C (PKC)-epsilon  
 CC activity higher than that of wild-type FVB/N epidermal cells. The  
 CC invention is useful for evaluating the effectiveness of a putative agent  
 CC as a chemopreventive agent against squamous cell carcinoma (SCC) disease in a  
 CC mammal by administering one putative agent to papilloma-suppressed FVB/N  
 CC mice having epidermal cells that comprise PKC-epsilon activity higher  
 CC than that of wild type FVB/N epidermal cells. The invention is also  
 CC useful as a tool for investigating the development of metastatic disease,  
 CC for screening putative agents for altering susceptibility, development  
 CC and progression of squamous cell carcinoma and metastatic squamous cell  
 CC carcinoma and as a model for the development and treatment of metastatic  
 CC skin cancer particularly squamous cell carcinoma in human and non-human  
 CC mammalian animals. The present sequence is mouse protein kinase C-epsilon  
 CC -T7 tag chimeric protein  
 CC  
 CC Sequence 737 AA;  
 SQ  
 Query Match 100.0%; Score 48; DB 7; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HDAPIGYD 8  
 Db 85 HDAPIGYD 92  
 RESULT 9  
 ADE57469  
 ID ADE57469 standard; protein; 737 AA.  
 XX  
 AC ADE57469;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein Q02156, SEQ ID NO 3331.  
 XX  
 KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNJ; Chung.  
 XX  
 OS Homo sapiens.  
 OS  
 PN W02003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0112147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GERO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'Urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; Q02156.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 737 AA;

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 10  
ADES7541  
ID ADE57541 standard; protein; 737 AA.  
XX  
AC ADE57541;

DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein Q02156, SEQ ID NO 3403.

XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX

OS Homo sapiens.

FN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

PI 2003-268312/26.

Position comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
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CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
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CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 737 AA;

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 11  
ADES8354  
ID ADE58354 standard; protein; 737 AA.  
XX  
AC ADE58354;

DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein Q02156, SEQ ID NO 4228.

XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX

OS Homo sapiens.

FN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

PI 2003-268312/26.

Position comprising two or more isolated polypeptides, useful for

XX WPI; 2003-268312/26.  
DR GENBANK; Q02156.  
XX  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
FT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
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XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
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CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 737 AA;  
SO

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 12  
ADE57531  
ID ADE57531 standard; protein; 737 AA.  
XX  
XX ADE57531;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Rat Protein AAA1872, SEQ ID NO 3393.  
DE  
XX  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
XX Rattus norvegicus.  
OS  
XX  
XX WO2003016475-A2.  
PN  
XX  
XX 27-FEB-2003.  
PD  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PE  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR  
XX  
XX 01-NOV-2001; 2001US-0346382P.  
PR  
XX  
XX 26-NOV-2001; 2001US-0333347P.  
XX

PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
FI  
XX  
XX WPI; 2003-268312/26.  
DR  
XX  
XX GENBANK; AAA1872.  
DR  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
FT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
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CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
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CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 737 AA;  
SO

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 13  
ADE57533  
ID ADE57533 standard; protein; 737 AA.  
XX  
XX ADE57533;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Human Protein Q02156, SEQ ID NO 3395.  
DE  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003016475-A2.  
PN  
XX  
XX 27-FEB-2003.  
PD  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX

XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX

PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX

PI Woolf C, D'urso D, Befort K, Costigan M;  
XX

DR WPI; 2003-268312/26.  
DR GENBANK; Q02156.  
XX

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX

PS Claim 1; Page: 1017pp; English.  
XX

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
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CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
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CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
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CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
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CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX

SQ Sequence 737 AA;  
XX

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 14  
ADES8352

ID ADE58352 standard; protein; 737 AA.  
XX

AC ADE58352;  
XX

DT 29-JAN-2004 (first entry)  
XX

DE Rat Protein KRTICE, SEQ ID NO 4226.  
XX

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX thus notreigicus.  
XX

016475-A2.

XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002MO-US025765.  
XX  
XX

PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX

PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX

PI Woolf C, D'urso D, Befort K, Costigan M;  
XX

DR WPI; 2003-268312/26.  
XX

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX

PS Claim 1; Page: 1017pp; English.  
XX

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
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CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
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CC the specification) which is differentially expressed during pain. Note:  
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CC ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX

SQ Sequence 737 AA;  
XX

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 15

ID ADE57535 standard; protein; 737 AA.  
XX

AC ADE57535;  
XX

DT 29-JAN-2004 (first entry)  
XX

DE Rat Protein AAA41872, SEQ ID NO 3397.  
XX

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX



OS Rattus norvegicus.  
 XX WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GHEO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 PI Woolf C, D'urso D, Befort K, Coetigan M;  
 XX WPI; 2003-268312/26.  
 DR GENBANK; AAA41872.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
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 CC The invention discloses a composition comprising two or more isolated rat  
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 CC that increases or decreases the expression of the polynucleotide sequence  
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 CC the expression of a polynucleotide sequence which is differentially  
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 CC activity in an animal of one or more of the polypeptides given in the  
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 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 737 AA;  
 QY  
 Query Match 100.0%; Score 48; DB 7; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 HDAPIGYD 8  
 65 HDAPIGYD 92  
 RESULT 16  
 ADE57537  
 ID ADE57537 standard; protein; 737 AA.  
 XX  
 XX ADE57537;  
 AC  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX Human Protein Q02156, SEQ ID NO 3399.  
 DE

XX Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX Homo sapiens.  
 XX WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GHEO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 PI Woolf C, D'urso D, Befort K, Coetigan M;  
 XX WPI; 2003-268312/26.  
 DR GENBANK; Q02156.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
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 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
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 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
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 XX  
 SQ Sequence 737 AA;  
 QY  
 Query Match 100.0%; Score 48; DB 7; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 HDAPIGYD 8  
 85 HDAPIGYD 92  
 RESULT 17  
 ADE57539  
 ID ADE57539 standard; protein; 737 AA.  
 XX

AC ADE57539;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Rat Protein AAA41872, SEQ ID NO 3401.  
DE  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
XX MO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'Urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
XX  
XX GENBANK; AAA41872.  
DR  
XX  
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PT preparing a medicament for treating pain in an animal.  
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XX  
XX Claim 1; Page; 1017pp; English.  
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CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 737 AA;  
SQ

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. NO. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18  
ADE57527  
ID ADE57527 standard; protein; 737 AA.  
XX  
XX AC ADE57527;  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX Rat Protein AAA41872, SEQ ID NO 3389.  
DE  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
XX Rattus norvegicus.  
XX  
XX OS  
XX  
XX MO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'Urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
XX  
XX GENBANK; AAA41872.  
DR  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX  
XX Claim 1; Page; 1017pp; English.  
PS  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 737 AA;  
SQ

Query Match 100.0%; Score 48; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. NO. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HDAPIGYD 8  
|||||||  
85 HDAPIGYD 92



## RESULT 21

ADY80138  
ID ADY80138 standard; protein; 737 AA.

XX AC ADY80138;

XX DT 02-JUN-2005 (first entry)

XX DE Amino acid sequence of murine protein kinase C epsilon.

XX KM protein kinase C epsilon; PKCε; glucose metabolism; insulin;

XX KW antidiabetic; protein kinase C epsilon antagonist;

XX KW non-insulin dependent diabetes; endocrine disease; hyperglycemia;

XX KW hyperinsulinemia; insulin resistance; glucose intolerance.

XX OS Mus sp.

XX PN MO2005025602-A1.

XX PD 24-MAR-2005.

XX PF 16-SEP-2004; 2004WO-AU001255.

XX PR 16-SEP-2003; 2003AU-00905421.

XX PR 22-JUL-2004; 2004AU-00904077.

XX PA (GARV-) GARVAN INST MEDICAL RES.

XX PI Biden TJ, Schmitz-Peiffer C;

XX PS WPI; 2005-253847/26.

XX DR N-PSDB; ADY80137.

XX DT Determining an antagonist of a protein kinase C epsilon (PKCε) for

XX PT treating abnormal glucose metabolism in subject comprises determining the

XX PT rate of internalization of the insulin receptor in the insulin-stimulated

XX PT hepatocytes.

XX PS Claim 8; SEQ ID NO 2; 138pp; English.

XX CC The specification describes a method for identifying modulators of

XX CC protein kinase C epsilon (PKCε) for the treatment of abnormal glucose

XX CC metabolism in a human or animal subject. The method comprises incubating

XX CC a hepatocyte in the presence and absence of a candidate compound;

XX CC stimulating the hepatocytes with insulin or its analogue; and determining

XX CC the rate of internalization of the insulin receptor in the insulin-

XX CC stimulated hepatocytes, where reduced insulin receptor internalization in

XX CC the presence of the candidate compound compared to in the absence of the

XX CC candidate compound indicates that the compound is an antagonist of PKCε.

XX CC The method is useful for treating abnormal glucose metabolism, e.g. Type

XX CC 2 diabetes, hyperglycemia, hyperinsulinemia, insulin resistance, or

XX CC glucose intolerance. The present sequence represents a murine PKCε.

XX SQ Sequence 737 AA;

Query Match 100.0%; Score 48; DB 9; Length 737;

Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8

DB 85 HDAPIGYD 92

## RESULT 22

ADY80140  
ID ADY80140 standard; protein; 737 AA.

XX AC ADY80140;

XX DT 02-JUN-2005 (first entry)

XX DE Amino acid sequence of human protein kinase C epsilon.

XX KM protein kinase C epsilon; PKCε; glucose metabolism; insulin;

XX KW antidiabetic; protein kinase C epsilon antagonist;

XX KW non-insulin dependent diabetes; endocrine disease; hyperglycemia;

XX KW hyperinsulinemia; insulin resistance; glucose intolerance.

XX OS Homo sapiens.

XX PN MO2005025602-A1.

XX PD 24-MAR-2005.

XX PF 16-SEP-2004; 2004WO-AU001255.

XX PR 16-SEP-2003; 2003AU-00905421.

XX PR 22-JUL-2004; 2004AU-00904077.

XX PA (GARV-) GARVAN INST MEDICAL RES.

XX PI Biden TJ, Schmitz-Peiffer C;

XX PS WPI; 2005-253847/26.

XX DR N-PSDB; ADY80139.

XX DT Determining an antagonist of a protein kinase C epsilon (PKCε) for

XX PT treating abnormal glucose metabolism in subject comprises determining the

XX PT rate of internalization of the insulin receptor in the insulin-stimulated

XX PT hepatocytes.

XX PS Example 8; SEQ ID NO 4; 138pp; English.

XX CC The specification describes a method for identifying modulators of

XX CC protein kinase C epsilon (PKCε) for the treatment of abnormal glucose

XX CC metabolism in a human or animal subject. The method comprises incubating

XX CC a hepatocyte in the presence and absence of a candidate compound;

XX CC stimulating the hepatocytes with insulin or its analogue; and determining

XX CC the rate of internalization of the insulin receptor in the insulin-

XX CC stimulated hepatocytes, where reduced insulin receptor internalization in

XX CC the presence of the candidate compound compared to in the absence of the

XX CC candidate compound indicates that the compound is an antagonist of PKCε.

XX CC The method is useful for treating abnormal glucose metabolism, e.g. Type

XX CC 2 diabetes, hyperglycemia, hyperinsulinemia, insulin resistance, or

XX CC glucose intolerance. The present sequence represents a human PKCε.

XX SQ Sequence 737 AA;

Query Match 100.0%; Score 48; DB 9; Length 737;

Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8

DB 85 HDAPIGYD 92

## RESULT 23

ADY80151  
ID ADY80151 standard; protein; 737 AA.

XX AC ADY80151;

XX DT 02-JUN-2005 (first entry)

XX DE Amino acid sequence of murine protein kinase C epsilon K437R mutant.

XX KM protein kinase C epsilon; PKCε; glucose metabolism; insulin;

XX KW antidiabetic; protein kinase C epsilon antagonist;

XX KW non-insulin dependent diabetes; endocrine disease; hyperglycemia;

XX KW hyperinsulinemia; insulin resistance; glucose intolerance.

XX OS Mus sp.

XX WO2005025602-A1.  
 PN 24-MAR-2005.  
 PD 16-SEP-2004; 2004WO-AU001255.  
 XX 16-SEP-2003; 2003AU-00905421.  
 XX 22-JUL-2004; 2004AU-00904077.  
 XX (GARV-) GARVAN INST MEDICAL RES.  
 PA Biden TJ, Schmitz-Peiffer C;  
 XX WPI, 2005-253847/26.  
 DR WPI, 2005-253847/26.  
 XX Determining an antagonist of a protein kinase C epsilon (PKCε) for  
 PT treating abnormal glucose metabolism in subject comprises determining the  
 PT rate of internalization of the insulin receptor in the insulin-stimulated  
 PT hepatocytes.  
 XX Claim 75; SEQ ID NO 15; 138bp; English.  
 PS The specification describes a method for identifying modulators of  
 CC protein kinase C epsilon (PKCε) for the treatment of abnormal glucose  
 CC metabolism in a human or animal subject. The method comprises incubating  
 CC a hepatocyte in the presence and absence of a candidate compound;  
 CC stimulating the hepatocytes with insulin or its analogue; and determining  
 CC the rate of internalization of the insulin receptor in the insulin-  
 CC stimulated hepatocytes, where reduced insulin receptor internalization in  
 CC the presence of the candidate compound compared to in the absence of the  
 CC candidate compound indicates that the compound is an antagonist of PKCε.  
 CC The method is useful for treating abnormal glucose metabolism, e.g. Type  
 CC 2 diabetes, hyperglycemia, hyperinsulinemia, insulin resistance, or  
 CC glucose intolerance. The present sequence encodes the murine PKCε K437R  
 CC mutant. This is a "kinase-dead" PKCε, which competes with wild type PKCε,  
 CC thereby competitively inhibiting the activity of endogenous PKCε in a  
 CC cell.  
 XX Sequence 737 AA;  
 SQ

Query Match 100.0%; Score 48; DB 9; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
 |||||  
 DB 85 HDAPIGYD 92

RESULT 24  
 ABB99506  
 ID ABB99506 standard; peptide; 8 AA.  
 XX ABB99506;  
 AC ABB99506;  
 XX 03-MAR-2003 (first entry)  
 DT Amino acid sequence of a modified pseudo-epsilon RACK peptide.  
 XX Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;  
 KW protein kinase C; PKC; tissue damage; ischaemia; hypoxia.  
 XX Synthetic.  
 OS WO200278600-A2.  
 XX WO200278600-A2.  
 PN 10-OCT-2002.  
 PD 10-OCT-2002.  
 XX 09-NOV-2001; 2001WO-US051600.  
 PF 10-NOV-2001; 2000US-0247830P.  
 PR 10-NOV-2001; 2000US-0247830P.  
 XX

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX Mochly-Rosen D;  
 PI WPI; 2003-092868/08.  
 DR WPI; 2003-092868/08.  
 XX New composition comprising pseudo-epsilonRACK peptides, useful for  
 PT treating tissue damage due to ischemia or hypoxia.  
 PT Claim 6; Page 13; 30pp; English.  
 PS The present sequence represents a modified pseudo-epsilon RACK  
 CC octapeptide (see also ABB99501). RACKs (receptors for activated C-kinase)  
 CC are anchoring molecules, which selectively anchor activated protein  
 CC kinase C (PKC) isozymes to their respective subcellular sites.  
 CC Compositions comprising pseudo-epsilon RACK peptides are useful for  
 CC reducing injury to a cell or tissue exposed to an ischemic or hypoxic  
 CC condition. The composition is useful for treating tissue damage due to  
 CC ischaemia or hypoxia  
 XX Sequence 8 AA;  
 SQ

Query Match 91.7%; Score 44; DB 6; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 2e+06;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
 |||||  
 DB 1 HDAPIGYE 8

RESULT 25  
 ABB99512  
 ID ABB99512 standard; peptide; 8 AA.  
 XX ABB99512;  
 AC ABB99512;  
 XX 03-MAR-2003 (first entry)  
 DT Amino acid sequence of a modified pseudo-epsilon RACK peptide.  
 XX Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;  
 KW protein kinase C; PKC; tissue damage; ischaemia; hypoxia.  
 XX Synthetic.  
 OS WO200278600-A2.  
 XX WO200278600-A2.  
 PN 10-OCT-2002.  
 PD 10-OCT-2002.  
 XX 09-NOV-2001; 2001WO-US051600.  
 PF 10-NOV-2001; 2000US-0247830P.  
 PR 10-NOV-2001; 2000US-0247830P.  
 XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA Mochly-Rosen D;  
 PI WPI; 2003-092868/08.  
 DR WPI; 2003-092868/08.  
 XX New composition comprising pseudo-epsilonRACK peptides, useful for  
 PT treating tissue damage due to ischemia or hypoxia.  
 PT Claim 6; Page 13; 30pp; English.  
 PS The present sequence represents a modified pseudo-epsilon RACK  
 CC octapeptide (see also ABB99501). RACKs (receptors for activated C-kinase)  
 CC are anchoring molecules, which selectively anchor activated protein  
 CC kinase C (PKC) isozymes to their respective subcellular sites.  
 CC Compositions comprising pseudo-epsilon RACK peptides are useful for  
 CC reducing injury to a cell or tissue exposed to an ischemic or hypoxic  
 CC condition. The composition is useful for treating tissue damage due to  
 CC ischaemia or hypoxia

XX Sequence 8 AA;  
SQ  
Query Match 91.7%; Score 44; DB 6; Length 8;  
Best Local Similarity 87.5%; Pred. No. 2e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 HDAPIGYD 8  
Db 1 HDGPIGYD 8

RESULT 26  
ABG76125  
ID ABG76125 standard; peptide; 8 AA.  
XX  
XX ABG76125;  
AC  
XX 07-MAY-2003 (first entry)  
DT  
XX  
XX Pepsilon RACK peptide #2.  
DE  
XX Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;  
KW receptor for activated C-kinase; myocardial infarction;  
KM cardiac ischaemia; pepsilon RACK.  
XX  
XX Synthetic.  
OS  
XX US2002168354-A1.  
PN  
XX 14-NOV-2002.  
PD  
XX 09-NOV-2001; 2001US-00007363.  
PE  
XX 10-NOV-2000; 2000US-0247830P.  
PR  
XX (MOCH/) MOCHLY-ROSEN D.  
PA  
XX Mochly-Rosen D;  
PI  
XX WPI; 2003-092868/08.  
DR  
XX  
XX New composition comprising pseudo-epsilonRACK peptides, useful for  
PT treating tissue damage due to ischemia or hypoxia.  
PT  
XX  
XX Claim 8; Page 6; 17pp; English.  
PS  
XX The invention relates to reducing injury to a cell or tissue exposed to  
CC an ischaemic or hypoxic condition, comprising administering to the cell  
CC or tissue a pepsilon Receptor for Activated C-Kinase (RACK) peptide.  
CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).  
CC The method is useful in treating or protecting cells and tissues from  
CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia  
CC or myocardial infarction. The present sequence is a pepsilon RACK  
CC peptide of the invention.  
CC  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 91.7%; Score 44; DB 6; Length 8;  
Best Local Similarity 87.5%; Pred. No. 2e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYE 8

RESULT 27  
ABG76131  
ABG76131 standard; peptide; 8 AA.  
76131;  
XX

DT 07-MAY-2003 (first entry)  
XX  
XX Pepsilon RACK peptide #8.  
DE  
XX Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;  
KW receptor for activated C-kinase; myocardial infarction;  
KM cardiac ischaemia; pepsilon RACK.  
XX  
XX Synthetic.  
OS  
XX US2002168354-A1.  
PN  
XX 14-NOV-2002.  
PD  
XX 09-NOV-2001; 2001US-00007363.  
PE  
XX 10-NOV-2000; 2000US-0247830P.  
PR  
XX (MOCH/) MOCHLY-ROSEN D.  
PA  
XX Mochly-Rosen D;  
PI  
XX WPI; 2003-092868/08.  
DR  
XX  
XX New composition comprising pseudo-epsilonRACK peptides, useful for  
PT treating tissue damage due to ischemia or hypoxia.  
PT  
XX  
XX Claim 8; Page 6; 17pp; English.  
PS  
XX The invention relates to reducing injury to a cell or tissue exposed to  
CC an ischaemic or hypoxic condition, comprising administering to the cell  
CC or tissue a pepsilon Receptor for Activated C-Kinase (RACK) peptide.  
CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).  
CC The method is useful in treating or protecting cells and tissues from  
CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia  
CC or myocardial infarction. The present sequence is a pepsilon RACK  
CC peptide of the invention.  
CC  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 91.7%; Score 44; DB 6; Length 8;  
Best Local Similarity 87.5%; Pred. No. 2e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 HDAPIGYD 8  
Db 1 HDGPIGYD 8

RESULT 28  
AEA89893  
ID AEA89893 standard; peptide; 8 AA.  
XX  
XX AEA89893;  
AC  
XX 08-SEP-2005 (first entry)  
DT  
XX  
XX Receptor for activated C kinase (RACK) peptide #15.  
DE  
XX  
XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;  
KW fibrosis; pulmonary fibrosis; septic shock; ischemia;  
KW inflammatory bowel disease; autoimmune disease; multiple sclerosis;  
KW Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;  
KW diabetes mellitus; pulmonary disease;  
KW chronic obstructive pulmonary disease; asthma;  
KW receptor for activated C kinase; RACK; antiinflammatory; dermatological;  
KW hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;  
KW antiproliferative; CNS-gen.; antithyroid; antirheumatic; antirheumatic;  
KW antidiabetic; antiaesthetic; gastrointestinal-gen.; antibacterial;  
KW vasotropic; cardiac.  
XX  
XX Homo sapiens.  
OS  
XX

PN WO2005059124-A2.  
 XX 30-JUN-2005.  
 PD 13-DEC-2004; 2004WO-US041854.  
 XX 11-DEC-2003; 2003US-0529223P.  
 PR (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA Mochly-Rosen D, Chen LE;  
 XX WPI; 2005-479333/48.  
 DR  
 XX  
 XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist  
 PT peptide useful for treating fibrotic or inflammatory disease, involves  
 PT substituting charged amino acid in agonist peptide with another uncharged  
 PT amino acid.  
 XX  
 PS Disclosure; SEQ ID NO 15; 90pp; English.  
 XX  
 CC The invention relates to a method of converting a protein kinase C (PKC)  
 CC agonist peptide or peptidomimetic to a PKC antagonist peptide or  
 CC peptidomimetic, involving substituting at least one amino acid in the  
 CC agonist peptide or peptidomimetic with an amino acid that converts the  
 CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or  
 CC peptidomimetic. The invention also relates to a method of inhibiting the  
 CC activity of a protein kinase C (PKC) enzyme, involving contacting the  
 CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide  
 CC derived from a PKC agonist peptide or peptidomimetic where at least one  
 CC amino acid in the agonist peptide or peptidomimetic is substituted with  
 CC another amino acid sufficient to convert the peptide or peptidomimetic  
 CC into an antagonist peptide or peptidomimetic. The method is useful for  
 CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist  
 CC peptide or peptidomimetic. The antagonist peptide is useful for treating  
 CC a disease or condition modulated by epsilon-PKC such as scleroderma,  
 CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory  
 CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre  
 CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes  
 CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease  
 CC and asthma. This sequence represents a receptor for activated C kinase  
 CC (RACK) peptide used in the method of the invention.  
 CC  
 XX  
 SQ Sequence 8 AA:  
 Query Match 91.7%; Score 44; DB 9; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 HDAPIGVD 8  
 Db 1 HDGPIGVD 8  
 RESULT 29  
 AEA89887  
 ID AEA89887 standard; peptide; 8 AA.  
 XX  
 AC AEA89887;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE Receptor for activated C kinase (RACK) peptide #9.  
 XX  
 KW Protein interaction; protein kinase C; epsilon-PKC; scleroderma;  
 KW fibrosis; pulmonary fibrosis; septic shock; ischemia;  
 KW inflammatory bowel disease; autoimmune disease; multiple sclerosis;  
 KW Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;  
 KW diabetes mellitus; pulmonary disease;  
 KW chronic obstructive pulmonary disease; asthma;  
 KW receptor for activated C kinase; RACK; antiinflammatory; dermatological;  
 KW hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;  
 KW antipeptidic; CNS-gen.; antihypoid; antiarthritic; antirheumatic;

KW antidiabetic; antisclastic; gastrointestinal-gen.; antibacterial;  
 KW vasotropic; cardiant.  
 XX  
 OS Homo sapiens.  
 XX WO2005059124-A2.  
 PN 30-JUN-2005.  
 PD 13-DEC-2004; 2004WO-US041854.  
 XX 11-DEC-2003; 2003US-0529223P.  
 PR (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA Mochly-Rosen D, Chen LE;  
 XX WPI; 2005-479333/48.  
 DR  
 XX  
 XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist  
 PT peptide useful for treating fibrotic or inflammatory disease, involves  
 PT substituting charged amino acid in agonist peptide with another uncharged  
 PT amino acid.  
 XX  
 PS Disclosure; SEQ ID NO 9; 90pp; English.  
 XX  
 CC The invention relates to a method of converting a protein kinase C (PKC)  
 CC agonist peptide or peptidomimetic to a PKC antagonist peptide or  
 CC peptidomimetic, involving substituting at least one amino acid in the  
 CC agonist peptide or peptidomimetic with an amino acid that converts the  
 CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or  
 CC peptidomimetic. The invention also relates to a method of inhibiting the  
 CC activity of a protein kinase C (PKC) enzyme, involving contacting the  
 CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide  
 CC derived from a PKC agonist peptide or peptidomimetic where at least one  
 CC amino acid in the agonist peptide or peptidomimetic is substituted with  
 CC another amino acid sufficient to convert the peptide or peptidomimetic  
 CC into an antagonist peptide or peptidomimetic. The method is useful for  
 CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist  
 CC peptide or peptidomimetic. The antagonist peptide is useful for treating  
 CC a disease or condition modulated by epsilon-PKC such as scleroderma,  
 CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory  
 CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre  
 CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes  
 CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease  
 CC and asthma. This sequence represents a receptor for activated C kinase  
 CC (RACK) peptide used in the method of the invention.  
 CC  
 XX  
 SQ Sequence 8 AA:  
 Query Match 91.7%; Score 44; DB 9; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 2e+06;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 HDAPIGVD 8  
 Db 1 HDGPIGVD 8  
 RESULT 30  
 AEA89909  
 ID AEA89909 standard; peptide; 8 AA.  
 XX  
 AC AEA89909;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE Receptor for activated C kinase (RACK) peptide #21.  
 XX  
 KW Protein interaction; protein kinase C; epsilon-PKC; scleroderma;  
 KW fibrosis; pulmonary fibrosis; septic shock; ischemia;  
 KW inflammatory bowel disease; autoimmune disease; multiple sclerosis;  
 KW Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;

KW diabetes mellitus; pulmonary disease;  
 KW chronic obstructive pulmonary disease; asthma;  
 KW receptor for activated C kinase; RACK; anti-inflammatory; dermatological;  
 KW hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;  
 KW antipneumatic; CNS-gen.; antichryoid; antiarthritic; antirheumatic;  
 KW antidiabetic; antiaesthetic; gastrointestinal-gen.; antibacterial;  
 KW vasotropic; cardiac.

OS Homo sapiens.

XX WO2005059124-A2.

XX 30-JUN-2005.

XX 13-DEC-2004; 2004WO-US041854.

XX 11-DEC-2003; 2003US-0529223P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D, Chen LE;

XX WPI; 2005-479333/48.

XX The invention relates to a method of converting a protein kinase C (PKC)  
 CC agonist peptide or peptidomimetic to a PKC antagonist peptide or  
 CC peptidomimetic, involving substituting at least one amino acid in the  
 CC agonist peptide or peptidomimetic with an amino acid that converts the  
 CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or  
 CC peptidomimetic. The invention also relates to a method of inhibiting the  
 CC activity of a protein kinase C (PKC) enzyme, involving contacting the  
 CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide  
 CC derived from a PKC agonist peptide or peptidomimetic where at least one  
 CC amino acid in the agonist peptide or peptidomimetic is substituted with  
 CC another amino acid sufficient to convert the peptide or peptidomimetic  
 CC into an antagonist peptide or peptidomimetic. The method is useful for  
 CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist  
 CC peptide or peptidomimetic. The antagonist peptide is useful for treating  
 CC a disease or condition modulated by epsilon-PKC such as scleroderma,  
 CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory  
 CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre  
 CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes  
 CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease  
 CC and asthma. This sequence represents a receptor for activated C kinase  
 CC (RACK) peptide used in the method of the invention.

XX Sequence 8 AA;

XX Query Match 91.7%; Score 44; DB 9; Length 8;  
 XX Best Local Similarity 87.5%; Pred. No. 2e+06;  
 XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
 XX |||||  
 DB 1 HDTPIGYD 8

RESULT 31

AAWS4889  
 ID AAWS4889 standard; peptide; 8 AA.

XX AAWS4889;

XX 1-SEP-1998 (first entry)

XX epsilon-specific agonist peptide epsilon VI-7.5.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.  
 KW Synthetic.  
 OS Synthetic.  
 XX WO9817299-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US018716.

XX 18-OCT-1996; 96US-0028724P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 1998-261181/23.

XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of  
 CC cells exposed to hypoxic conditions.

XX Disclosure; Page 32; 47pp; English.

XX The peptides AAWS4879-W54901 are agonists of epsilon protein kinase C  
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed  
 CC to hypoxic conditions. They can also be used in a method for identifying  
 CC a compound effective to induce preconditioning. The peptides are  
 CC administered at a dose of 1-100 microgram administered once to several  
 CC times daily in bolus injections

XX Sequence 8 AA;

XX Query Match 89.6%; Score 43; DB 2; Length 8;  
 XX Best Local Similarity 87.5%; Pred. No. 2e+06;  
 XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
 XX |||||  
 DB 1 HNAPIGYD 8

RESULT 32

AAWS4892  
 ID AAWS4892 standard; peptide; 8 AA.

XX AAWS4892;

XX 24-SEP-1998 (first entry)

XX Isozyme-specific agonist peptide epsilon VI-7.8.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.

XX Synthetic.

XX WO9817299-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US018716.

XX 18-OCT-1996; 96US-0028724P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 1998-261181/23.

XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of  
 PT cells exposed to hypoxic conditions.



PS Claim 1; Page 32; 47pp; English.

XX The peptides AAW54879-W54901 are agonists of epsilon protein kinase C  
CC (PKC). They can be used for reducing ischaemic injury to a cell exposed  
CC to hypoxic conditions. They can also be used in a method for identifying  
CC a compound effective to induce preconditioning. The peptides are  
CC administered at a dose of 1-100 microgram administered once to several  
CC times daily in bolus injections

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 2; Length 8;

Best Local Similarity 87.5%; Pred. No. 2e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPICGYD 8  
Db 1 HDAPAGYD 8

RESULT 33

ABB99507  
ID ABB99507 standard; peptide; 8 AA.

XX ABB99507;

XX 03-MAR-2003 (first entry)

XX Amino acid sequence of a modified pseudo-epsilon RACK peptide.

XX Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;  
KW protein kinase C; PKC; tissue damage; ischaemia; hypoxia.

XX Synthetic.

XX WO200278600-A2.

XX 10-OCT-2002.

XX 09-NOV-2001; 2001WO-US051600.

XX 10-NOV-2000; 2000US-0247830P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 2003-092868/08.

XX New composition comprising pseudo-epsilonRACK peptides, useful for  
PT treating tissue damage due to ischemia or hypoxia.

XX Claim 6; Page 13; 30pp; English.

XX The present sequence represents a modified pseudo-epsilon RACK  
CC octapeptide (see also ABB99501). RACKs (receptors for activated C-kinase)  
CC are anchoring molecules, which selectively anchor activated protein  
CC kinase C (PKC) isozymes to their respective subcellular sites.  
CC Compositions comprising pseudo-epsilon RACK peptides are useful for  
CC reducing injury to a cell or tissue exposed to an ischaemic or hypoxic  
CC condition. The composition is useful for treating tissue damage due to  
CC ischaemia or hypoxia

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 6; Length 8;

Best Local Similarity 75.0%; Pred. No. 2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPICGYD 8  
Db 1 HDAPAGYE 8

RESULT 34

ABG76126  
ID ABG76126 standard; peptide; 8 AA.

XX ABG76126;

XX 07-MAY-2003 (first entry)

XX Psepsilon RACK peptide #3.

XX Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;  
KW receptor for activated C-kinase; myocardial infarction;  
KW cardiac ischaemia; psepsilon RACK.

XX Synthetic.

XX US2002168354-A1.

XX 14-NOV-2002.

XX 09-NOV-2001; 2001US-00007363.

XX 10-NOV-2000; 2000US-0247830P.

XX (MOCH/) MOCHLY-ROSEN D.

XX Mochly-Rosen D;

XX WPI; 2003-092868/08.

XX New composition comprising pseudo-epsilonRACK peptides, useful for  
PT treating tissue damage due to ischemia or hypoxia.

XX Claim 8; Page 6; 17pp; English.

XX The invention relates to reducing injury to a cell or tissue exposed to  
CC an ischaemic or hypoxic condition, comprising administering to the cell  
CC or tissue a psepsilon Receptor for Activated C-kinase (RACK) peptide.  
CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).  
CC The method is useful in treating or protecting cells and tissues from  
CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia  
CC or myocardial infarction. The present sequence is a psepsilon RACK  
CC peptide of the invention

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 6; Length 8;

Best Local Similarity 75.0%; Pred. No. 2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPICGYD 8  
Db 1 HDAPVGYE 8

RESULT 35

AEA89933  
ID AEA89933 standard; peptide; 8 AA.

XX AEA89933;

XX 08-SEP-2005 (first entry)

XX Receptor for activated C kinase (RACK) peptide #55.

XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;  
KW fibrosis; pulmonary fibrosis; septic shock; ischemia;  
KW inflammatory bowel disease; autoimmune disease; multiple sclerosis;  
KW Guillain Barre syndrome; psoriasis; Graves disease; Rheumatoid arthritis;  
KW diabetes mellitus; pulmonary disease;  
KW chronic obstructive pulmonary disease; asthma;  
KW receptor for activated C kinase; RACK; antiinflammatory; dermatological;

KM	hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;
KM	antipneumonic; CNS-gen.; antithyroid; antirheumatic; antihemagic;
KM	antidiabetic; antiaesthetic; gastrointestinal-gen.; antibacterial;
KM	vasotropic; cardiac.
XX	
OS	Homo sapiens.
XX	
PN	MO2005059124-A2.
XX	
PD	30-JUN-2005.
XX	
PF	13-DEC-2004; 2004MO-US041854.
XX	
PR	11-DEC-2003; 2003US-0529223P.
XX	
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.
XX	
PI	Mochly-Rosen D, Chen LE;
XX	
DR	WPI; 2005-479333/48.
XX	
PT	Converting protein kinase C (PKC) agonist peptide to PKC antagonist
PT	peptide useful for treating fibrotic or inflammatory disease, involves
PT	substituting charged amino acid in agonist peptide with another uncharged
PT	amino acid.

Query Match	89.6%	Score 43	DB 9	Length 8
Best Local Similarity	87.5%	Pred. No. 2e+05		
Matches 7	Conservative	1	Mismatches 0	Indels 0
			Gaps	0

QY	1	HDAPIGYD	8
		:	
Db	1	HNAPIGYD	8

```

RESULT 36
AEA89888
ID AEA89888 standard; peptide; 8 AA
XX
AC AEA89888;
XX
DT 08-SEP-2005 (first entry)
..

```

protein interaction; protein kinase C; epsilon-PKC; scleroderma; cysts; pulmonary fibrosis; septic shock; ischemia;

XX	inflammatory bowel disease; autoimmune disease; multiple sclerosis;
KM	Gullain Barre syndrome; poriasis; Graves disease; rheumatoid arthritis;
XX	diabetes mellitus; pulmonary disease;
KM	chronic obstructive pulmonary disease; asthma;
KM	receptor for activated C kinase; RACK; antiinflammatory; dermatological;
KM	hepatocellular; respiratory-gen.; immunosuppressive; neuroprotective;
XX	antibiotic; Csp-Gen.; antichryoid; antiarthritic; antirheumatic;
KM	antidiabetic; antiaesthetic; gastrointestinal-gen.; antibacterial;
XX	vasotropic; cardiant.
XX	
OS	Homo sapiens.
XX	
PN	MO2005059124-A2.
XX	
PD	30-JUN-2005.
XX	
PF	13-DEC-2004; 2004WO-US041854.
XX	
PR	11-DEC-2003; 2003US-0529223P.
XX	
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.
XX	
XX	
XX	Mochly-Rosen D, Chen LE;
DR	WPI; 2005-479333/48.
XX	
XX	Converting protein kinase C (PKC) agonist peptide to PKC antagonist
PT	peptide useful for treating fibrotic or inflammatory disease, involves
PT	substituting charged amino acid in agonist peptide with another uncharged
PT	amino acid.

Query Match	89.6%	Score 43	DB 9	Length 8
Best Local Similarity	75.0%	Pred. No. 2e+06		
Matches 6, Conservative		2, Mismatches	0, Indels	0, Gaps

Qy	1	HDAPIGYD	8
		:	
Db	1	HDAPVGYE	8

```

RESULT 37
AAW54894
ID AAW54894 standard; peptide; 8 AA
XX
XX AAW54894;
XX
XX
DT 24-SEP-1998 (first entry)

```

XX Isozyme-specific agonist peptide epsilon VI-7.10.  
XX  
XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.  
XX  
XX Synthetic.  
XX  
XX WO9817299-A1.  
XX  
XX 30-APR-1998.  
XX  
XX  
XX 17-OCT-1997; 97WO-US018716.  
XX  
XX 18-OCT-1996; 96US-0028724P.  
XX  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
XX Mochly-Rosen D;  
XX  
XX WPI; 1998-261181/23.  
XX  
XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of  
XX cells exposed to hypoxic conditions.  
XX  
XX Claim 1; Page 32; 47pp; English.  
XX  
XX The peptides AAW54879-W54901 are agonists of epsilon protein kinase C  
XX (PKC). They can be used for reducing ischaemic injury to a cell exposed  
XX to hypoxic conditions. They can also be used in a method for identifying  
XX a compound effective to induce preconditioning. The peptides are  
XX administered at a dose of 1-100 microgram administered once to several  
XX times daily in bolus injections  
XX  
XX Sequence 8 AA;  
SQ

Query Match 87.5%; Score 42; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 2e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAP1AYD 8

## RESULT 38

AAW54895  
ID AAW54895 standard; peptide; 8 AA.

XX AAW54895;

XX 24-SEP-1998 (first entry)

XX Isozyme-specific agonist peptide epsilon VI-7.11.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.

XX Synthetic.

XX WO9817299-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US018716.

XX 18-OCT-1996; 96US-0028724P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 1998-261181/23.

XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of

PT cells exposed to hypoxic conditions.

XX Claim 1; Page 32; 47pp; English.

XX The peptides AAW54879-W54901 are agonists of epsilon protein kinase C

XX (PKC). They can be used for reducing ischaemic injury to a cell exposed

XX to hypoxic conditions. They can also be used in a method for identifying

XX a compound effective to induce preconditioning. The peptides are

XX administered at a dose of 1-100 microgram administered once to several

XX times daily in bolus injections

XX Sequence 8 AA;  
SQ

QY 1 HDAPIGY 7  
Db 1 HDAP1GY 7

RESULT 39  
ABB99508  
ID ABB99508 standard; peptide; 8 AA.

XX ABB99508;

XX 03-MAR-2003 (first entry)

XX Amino acid sequence of a modified pseudo-epsilon RACK peptide.

XX Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;

XX protein kinase C; PKC; tissue damage; ischaemia; hypoxia.

XX Synthetic.

XX WO200278600-A2.

XX 10-OCT-2002.

XX 09-NOV-2001; 2001WO-US051600.

XX 10-NOV-2000; 2000US-0247830P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 2003-092868/08.

XX New composition comprising pseudo-epsilonRACK peptides, useful for

XX treating tissue damage due to ischemia or hypoxia.

XX Claim 6; Page 13; 30pp; English.

XX The present sequence represents a modified pseudo-epsilon RACK

XX octapeptide (see also ABB99501). RACKs (receptors for activated C-kinase)

XX are anchoring molecules, which selectively anchor activated protein

XX kinase C (PKC) isozymes to their respective subcellular sites.

XX Compositions comprising pseudo-epsilon RACK peptides are useful for

XX reducing injury to a cell or tissue exposed to an ischaemic or hypoxic

XX condition. The composition is useful for treating tissue damage due to

XX ischaemia or hypoxia  
QY 1 HDAPIGYD 8  
Db 1 HDAP1GYD 8

SQ

Query Match 87.5%; Score 42; DB 6; Length 8;

Best Local Similarity 75.0%; Pred. No. 2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 HDAPLGYE 8

## RESULT 40

ABG76127  
ID ABG76127 standard; peptide; 8 AA.

XX ABG76127;

XX AC  
XX DT 07-MAY-2003 (first entry)

XX DE Psepleton RACK peptide #4.

XX Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;  
KW receptor for activated C-kinase; myocardial infarction;  
KW cardiac ischaemia; psepleton RACK.

XX OS Synthetic.

XX PN US2002168354-A1.

XX PD 14-NOV-2002.

XX PF 09-NOV-2001; 2001US-00007363.

XX PR 10-NOV-2000; 2000US-0247830P.

XX PA (MOCH/) MOCHLY-ROSEN D.

XX PI Mochly-Rosen D;

XX DR WPI; 2003-092868/08.

XX PT New composition comprising pseudo-epsilonRACK peptides, useful for  
XX treating tissue damage due to ischemia or hypoxia.

XX PS Claim 8; Page 6; 17pp; English.

XX CC The invention relates to reducing injury to a cell or tissue exposed to  
XX an ischaemic or hypoxic condition, comprising administering to the cell  
XX or tissue a psepleton Receptor for Activated C-Kinase (RACK) peptide.

XX CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).

XX CC The method is useful in treating or protecting cells and tissues from  
XX damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia  
XX or myocardial infarction. The present sequence is a psepleton RACK  
XX peptide of the invention

SQ Sequence 8 AA;

Query Match 87.5%; Score 42; DB 6; Length 8;

Best Local Similarity 75.0%; Pred. No. 2e+06;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
|||:|:

Db 1 HDAPLGYE 8

Search completed: December 3, 2005, 23:28:01  
Job time : 189 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:23:33 ; Search time 24 Seconds  
(without alignments)  
27.559 Million cell updates/sec

Title: US-10-807-553-2  
Perfect score: 48  
Sequence: 1 HDAPIGVD 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCrUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	8	US-08-953-033-6	Sequence 6, Appli
2	48	100.0	156	US-09-771-161A-104	Sequence 104, App
3	48	100.0	737	US-09-772-647-4	Sequence 4, Appli
4	48	100.0	737	US-10-228-931-4	Sequence 4, Appli
5	48	100.0	737	US-09-771-161A-195	Sequence 195, App
6	43	89.6	8	US-08-953-033-11	Sequence 11, Appli
7	43	89.6	8	US-08-953-033-14	Sequence 14, Appli
8	42	87.5	8	US-08-953-033-16	Sequence 16, Appli
9	42	87.5	8	US-08-953-033-17	Sequence 17, Appli
10	42	87.5	11	US-08-594-447-19	Sequence 19, Appli
11	42	87.5	11	US-08-541-964-18	Sequence 18, Appli
12	42	87.5	11	US-08-665-647-33	Sequence 33, Appli
13	40	83.3	8	US-08-953-033-9	Sequence 9, Appli
14	40	83.3	8	US-08-953-033-10	Sequence 10, Appli
15	40	83.3	8	US-08-953-033-12	Sequence 12, Appli
16	40	83.3	8	US-08-953-033-13	Sequence 13, Appli
17	39	81.2	8	US-08-953-033-15	Sequence 15, Appli
18	38	79.2	8	US-08-953-033-20	Sequence 20, Appli
19	38	79.2	682	US-09-538-092-1003	Sequence 1003, Ap
20	38	79.2	739	US-09-949-016-7606	Sequence 7606, Ap
21	37.5	78.1	14	US-08-953-033-23	Sequence 23, Appli
22	35	72.9	8	US-08-953-033-8	Sequence 8, Appli
23	35	72.9	6	US-08-953-033-7	Sequence 7, Appli
24	35	72.9	14	US-09-747-287A-207	Sequence 207, App
25	35	72.9	14	US-09-394-019C-156	Sequence 156, App
26	35	72.9	14	US-09-394-019C-253	Sequence 253, App
27	35	72.9	14	US-09-394-019C-401	Sequence 401, App

28	72.9	361	2	US-09-949-016-11594	Sequence 11594, A
29	72.9	374	2	US-09-489-039A-7383	Sequence 7383, Ap
30	72.9	480	2	US-09-252-991A-26250	Sequence 26250, A
31	72.9	649	2	US-09-134-001C-3891	Sequence 3891, Ap
32	70.8	10	1	US-08-584-226-22	Sequence 22, Appli
33	70.8	16	2	US-09-747-287A-91	Sequence 91, Appli
34	70.8	16	2	US-09-747-287A-92	Sequence 92, Appli
35	70.8	16	2	US-09-747-287A-93	Sequence 93, Appli
36	70.8	16	2	US-09-747-287A-206	Sequence 206, App
37	70.8	18	2	US-09-747-287A-94	Sequence 94, Appli
38	70.8	18	2	US-09-747-287A-95	Sequence 95, Appli
39	70.8	18	2	US-09-747-287A-96	Sequence 96, Appli
40	70.8	18	2	US-09-747-287A-97	Sequence 97, Appli
41	70.8	18	2	US-09-747-287A-98	Sequence 98, Appli
42	70.8	18	2	US-09-747-287A-99	Sequence 99, Appli
43	70.8	18	2	US-09-747-287A-204	Sequence 204, App
44	70.8	183	2	US-09-270-767-34573	Sequence 34573, A
45	70.8	163	2	US-09-270-767-49790	Sequence 49790, A
46	70.8	245	2	US-09-902-540-13549	Sequence 13549, A
47	70.8	340	2	US-09-270-767-58348	Sequence 58348, A
48	70.8	477	2	US-09-270-767-43020	Sequence 43020, A
49	70.8	483	2	US-09-543-681A-5752	Sequence 5752, Ap
50	70.8	500	2	US-09-325-932A-149	Sequence 149, App
51	70.8	554	2	US-09-198-452A-140	Sequence 140, App
52	70.8	554	2	US-09-438-185A-124	Sequence 124, App
53	70.8	659	2	US-09-392-772-10	Sequence 10, Appli
54	70.8	680	2	US-09-252-991A-17566	Sequence 17566, A
55	70.8	683	2	US-09-543-681A-5403	Sequence 5403, Ap
56	70.8	703	2	US-09-902-540-10686	Sequence 10686, A
57	70.8	716	2	US-09-489-039A-8243	Sequence 8243, Ap
58	70.8	720	2	US-09-328-352-4765	Sequence 4765, Ap
59	70.8	1131	2	US-09-487-5588-72	Sequence 72, Appli
60	68.8	262	1	US-08-602-359A-35	Sequence 35, Appli
61	68.8	488	2	US-09-489-039A-7965	Sequence 7965, Ap
62	68.8	690	2	US-09-540-236-3507	Sequence 3507, Ap
63	66.7	11	1	US-08-594-447-26	Sequence 26, Appli
64	66.7	11	1	US-08-541-964-25	Sequence 25, Appli
65	66.7	11	1	US-08-665-647-40	Sequence 40, Appli
66	66.7	102	1	US-07-901-703-5	Sequence 5, Appli
67	66.7	102	1	US-08-278-729A-11	Sequence 11, Appli
68	66.7	102	1	US-08-155-343A-11	Sequence 11, Appli
69	66.7	102	1	US-08-406-672-11	Sequence 11, Appli
70	66.7	102	1	US-08-335-583C-50	Sequence 50, Appli
71	66.7	102	1	US-08-643-563A-11	Sequence 11, Appli
72	66.7	102	1	US-08-643-763A-11	Sequence 11, Appli
73	66.7	102	1	US-08-462-623-11	Sequence 11, Appli
74	66.7	102	1	US-08-451-953A-11	Sequence 11, Appli
75	66.7	102	1	US-08-445-468A-11	Sequence 11, Appli
76	66.7	102	1	US-08-461-397A-11	Sequence 11, Appli
77	66.7	102	1	US-08-912-088-11	Sequence 11, Appli
78	66.7	102	2	US-08-278-730A-11	Sequence 11, Appli
79	66.7	102	2	US-08-478-097A-6	Sequence 6, Appli
80	66.7	102	2	US-08-445-467-11	Sequence 11, Appli
81	66.7	102	2	US-08-480-515A-11	Sequence 11, Appli
82	66.7	102	2	US-08-414-033A-11	Sequence 11, Appli
83	66.7	102	2	US-08-271-556A-9	Sequence 9, Appli
84	66.7	102	2	US-08-931-858E-158	Sequence 158, App
85	66.7	102	2	US-08-981-739-158	Sequence 158, App
86	66.7	102	2	US-08-440-894A-11	Sequence 11, Appli
87	66.7	102	2	US-09-170-93A-11	Sequence 11, Appli
88	66.7	102	2	US-08-461-113-11	Sequence 11, Appli
89	66.7	102	2	US-09-128-026-158	Sequence 158, App
90	66.7	102	2	US-09-426-398-6	Sequence 6, Appli
91	66.7	102	2	US-08-456-033-11	Sequence 11, Appli
92	66.7	102	2	US-08-643-321-10	Sequence 10, Appli
93	66.7	102	2	US-09-464-206-11	Sequence 11, Appli
94	66.7	102	2	US-08-404-113A-11	Sequence 11, Appli
95	66.7	102	2	US-09-220-616-158	Sequence 158, App
96	66.7	102	2	US-09-374-958C-45	Sequence 45, Appli
97	66.7	102	2	US-09-220-527-158	Sequence 158, App
98	66.7	102	2	US-09-220-407-158	Sequence 158, App
99	66.7	102	2	US-08-260-675-11	Sequence 11, Appli
100	66.7	102	2	US-09-374-936-45	Sequence 45, Appli

## ALIGNMENTS

RESULT 1  
US-08-953-033-6  
Sequence 6, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF INVENTION: 23  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESS: Dellinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pettibony, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLSCULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilon-PKC residues 85-92; epsilonV1-7; E7  
US-08-953-033-6

Query Match  
Best Local Similarity 100.0%; Score 48; DB 2; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 2  
US-09-771-161A-104  
Sequence 104, Application US/09771161A  
Patent No. 6936450  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 104  
LENGTH: 156  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-104

Query Match  
Best Local Similarity 100.0%; Score 48; DB 2; Length 156;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 3  
US-09-772-647-4  
Sequence 4, Application US/09772647  
Patent No. 6521815  
GENERAL INFORMATION:  
APPLICANT: Verma, Ajit K  
APPLICANT: Reddig, Peter J  
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma  
FILE REFERENCE: 960296.97613  
CURRENT APPLICATION NUMBER: US/09/772,647  
CURRENT FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 737  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and  
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence  
US-09-772-647-4

Query Match  
Best Local Similarity 100.0%; Score 48; DB 2; Length 737;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 4  
US-10-228-931-4  
Sequence 4, Application US/10228931  
Patent No. 6897352  
GENERAL INFORMATION:  
APPLICANT: Verma, Ajit K  
APPLICANT: Reddig, Peter J  
APPLICANT: Jansen, Aaron P  
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma  
FILE REFERENCE: 960296.97613  
CURRENT APPLICATION NUMBER: US/10/228,931  
CURRENT FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: US/09/772,647  
PRIOR FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4

LENGTH: 737  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and  
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence  
US-10-228-931-4

Query Match 100.0%; Score 48; DB 2; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0.48; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 5  
US-09-771-161A-195  
Sequence 195, Application US/09771161A  
Patent No. 6936450  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
PRIORITY FILING DATE: 2001-01-26  
PRIORITY APPLICATION NUMBER: 09/724,676  
PRIORITY FILING DATE: 2000-11-28  
PRIORITY APPLICATION NUMBER: 136776  
PRIORITY FILING DATE: 2000-06-15  
PRIORITY APPLICATION NUMBER: 135619  
PRIORITY FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 195  
LENGTH: 737  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-195

Query Match 100.0%; Score 48; DB 2; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0.48; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 6  
US-08-953-033-11  
Sequence 11, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pelthoroy, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilonH1-7.5  
US-08-953-033-11

Query Match 89.6%; Score 43; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 4.6e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HNDAPIGYD 8

RESULT 7  
US-08-963-033-14  
Sequence 14, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pelthoroy, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:

;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURES:  
;; NAME/KEY: Other  
;; LOCATION: 1...8  
;; OTHER INFORMATION: epsilonV1-7.8  
US-08-953-033-14

Query Match 89.5%; Score 43; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPAGYD 8

RESULT 8  
US-08-953-033-16  
Sequence 16, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Delinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petichory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURES:  
NAME/KEY: No. 6165977e  
LOCATION: 1...8  
OTHER INFORMATION: epsilonV1-7.10  
-033-16

Best Local Similarity 87.5%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPAGYD 8

RESULT 9  
US-08-953-033-17  
Sequence 17, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Delinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petichory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURES:  
NAME/KEY: No. 6165977e  
LOCATION: 1...8  
OTHER INFORMATION: epsilonV1-7.11  
US-08-953-033-17

Query Match 87.5%; Score 42; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGY 7  
Db 1 HDAPIGY 7

RESULT 10  
US-08-594-447-19  
Sequence 19, Application US/08594447  
Patent No. 5776716  
GENERAL INFORMATION:  
APPLICANT: Ron, Dorit



APPLICANT: Napolitano, Eugene W.  
APPLICANT: Voronova, Anna F.  
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH  
BLOCK THE INTERACTION OF PYN WITH PKC-THETA, AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,447  
FILING DATE: 31-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..11  
OTHER INFORMATION: /label= epsilon-VI-3  
US-08-594-447-19  
Query Match 87.5%; Score 42; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.083;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HDAPIGY 7  
Db 5 HDAPIGY 11  
RESULT 11  
US-08-541-964-18  
Sequence 18, Application US/08541964  
Patent No. 5783405  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Ron, Dorit  
APPLICANT: Kavaar, Lawrence M.  
APPLICANT: Napolitano, Eugene W.  
TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,964  
FILING DATE: 10-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.23  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..11  
OTHER INFORMATION: /label= epsilon-VI-3  
US-08-541-964-18  
Query Match 87.5%; Score 42; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.083;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HDAPIGY 7  
Db 5 HDAPIGY 11  
RESULT 12  
US-08-665-647-33  
Sequence 33, Application US/08665647  
Patent No. 593803  
GENERAL INFORMATION:  
APPLICANT: Daeguez, Nicki J.  
APPLICANT: Ron, Dorit  
APPLICANT: Voronova, Anna F.  
APPLICANT: Napolitano, Eugene W.  
TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS  
USING COGNATE INTERACTION OF PKC-THETA  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,647  
FILING DATE: 18-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.25  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168  
TELEX: 90-4030 MRSNFOERSWSH

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..11  
OTHER INFORMATION: /label= epsilon-VI-3  
US-08-665-647-33

Query Match 87.5%; Score 42; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.083;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7  
Db 5 HDAPIGY 11

RESULT 13  
US-08-953-033-9  
Sequence 9, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
TITLE OF INVENTION: POSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESS: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953.033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pelichory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilon-VI-7.3  
US-08-953-033-9

Query Match 83.3%; Score 40; DB 2; Length 8;

Best Local Similarity 87.5%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 14  
US-08-953-033-10  
Sequence 10, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
TITLE OF INVENTION: POSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESS: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953.033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pelichory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilon-VI-7.4  
US-08-953-033-10

Query Match 83.3%; Score 40; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 15  
US-08-953-033-12  
Sequence 12, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
TITLE OF INVENTION: POSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953.033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilonV1-7.6  
US-08-953-033-12

Query Match 83.3%; Score 40; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGVD 8  
Db 1 HAAPIGVD 8

RESULT 16  
US-08-953-033-13  
Sequence 13, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953.033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilonV1-7.7  
US-08-953-033-13

Query Match 83.3%; Score 40; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGVD 8  
Db 2 DAPIGVD 8

RESULT 17  
US-08-953-033-15  
Sequence 15, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953.033  
FILING DATE: 17-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilon1-7.9  
US-08-953-033-15

Query Match 81.2% Score 39; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 4.6e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGAD 8

RESULT 18  
US-08-953-033-20  
Sequence 20, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF INVENTION: POSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953.033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: nvl-7

US-08-953-033-20

Query Match 79.2% Score 38; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HETPLGYD 8

RESULT 19  
US-09-538-092-1003  
Sequence 1003, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Glot, Loic  
APPLICANT: Mansfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538.092  
CURRENT FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CuratSeqFormatter Version 0.9  
SEQ ID NO 1003  
LENGTH: 682  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Polypeptide Accession Number P24723  
US-09-538-092-1003

Query Match 79.2% Score 38; DB 2; Length 682;  
Best Local Similarity 62.5%; Pred. No. 37;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 88 HETPLGYD 95

RESULT 20  
US-09-949-016-7606  
Sequence 7606, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT APPLICATION NUMBER: US/09/949.016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7606  
LENGTH: 739  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7606

Query Match 79.2% Score 38; DB 2; Length 739;

Best Local Similarity 62.5%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 HDAPIGVD 8  
Db 144 HETPLGVD 151

## RESULT 21

US-08-953-033-23  
Sequence 23, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF INVENTION: POSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Delinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...14  
OTHER INFORMATION: epsilonV1-7.1x  
US-08-953-033-23

Query Match 78.1%; Score 37.5; DB 2; Length 14;  
Best Local Similarity 88.9%; Pred. No. 0.78;  
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 HDAPIGVD 8  
Db 4 HDAPIGVD 12

## RESULT 22

US-08-953-033-8  
Sequence 8, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
TITLE OF INVENTION: POSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Delinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...6  
OTHER INFORMATION: epsilonV1-7.2  
US-08-953-033-8

Query Match 72.9%; Score 35; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIG 6  
Db 1 HDAPIG 6

## RESULT 23

US-08-953-033-7  
Sequence 7, Application US/08953033  
Patent No. 6165977  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS  
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM  
NUMBER OF INVENTION: POSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Delinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/953,033  
FILING DATE: 17-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,724  
FILING DATE: 18-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pettiberty, Joanne R.  
REGISTRATION NUMBER: 42,995  
REFERENCE/DOCKET NUMBER: 8600-0174.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...8  
OTHER INFORMATION: epsilonY1-7.1  
US-08-953-033-7

Query Match 72.9%; Score 35; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6  
Db 1 HDAPIG 6

RESULT 24  
US-09-747-287A-207  
Sequence 207, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
APPLICANT: PACKARD, BEVERLY S.  
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 207  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide.  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (4)..(4)  
OTHER INFORMATION: Xaa is epsilon-aminoacaproic acid  
US-09-747-287A-207

Query Match 72.9%; Score 35; DB 2; Length 14;  
Best Local Similarity 85.7%; Pred. No. 2.4;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 HDAPIG 7  
Db 8 HDAPKGY 14

RESULT 25  
US-09-394-019C-156  
Sequence 156, Application US/09394019C  
Patent No. 6936687  
GENERAL INFORMATION:  
APPLICANT: OncoImmunin, Inc.  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly  
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
FILE REFERENCE: 300-903820US  
CURRENT APPLICATION NUMBER: US/09/394,019C  
CURRENT FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: PCT/US98/00300  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 08/802,981  
PRIOR FILING DATE: 1997-02-20  
NUMBER OF SEQ ID NOS: 405  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 156  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide substrate  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)-(1)  
OTHER INFORMATION: K is blocked with Fmoc  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4)..(4)  
OTHER INFORMATION: X is epsilon aminoacaproic acid  
US-09-394-019C-156

Query Match 72.9%; Score 35; DB 2; Length 14;  
Best Local Similarity 85.7%; Pred. No. 2.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7  
Db 8 HDAPKGY 14

RESULT 26  
US-09-394-019C-253  
Sequence 253, Application US/09394019C  
Patent No. 6936687  
GENERAL INFORMATION:  
APPLICANT: OncoImmunin, Inc.  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly  
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
FILE REFERENCE: 300-903820US  
CURRENT APPLICATION NUMBER: US/09/394,019C  
CURRENT FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: PCT/US98/00300  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 08/802,981  
PRIOR FILING DATE: 1997-02-20  
NUMBER OF SEQ ID NOS: 405

SOFTWARE: Patentin version 3.2  
; SEQ ID NO 253  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide substrate  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: X is epsilon-aminocaproic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-09-394-019C-253

Query Match 72.9%; Score 35; DB 2; Length 14;  
Best Local Similarity 85.7%; Pred. No. 2.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7  
Db 8 HDAPKGY 14

RESULT 27  
US-09-394-019C-401  
; Sequence 401, Application US/09394019C  
; Patent No. 6936687  
; GENERAL INFORMATION:  
; APPLICANT: Oncolimmunh, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
; FILE REFERENCE: 300-903820US  
; CURRENT APPLICATION NUMBER: US/09/394,019C  
; CURRENT FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 405  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 401  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide. Chemically synthesized protease substrate.  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid  
US-09-394-019C-401

Query Match 72.9%; Score 35; DB 2; Length 14;  
Best Local Similarity 85.7%; Pred. No. 2.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7  
Db 8 HDAPKGY 14

RESULT 28  
US-09-949-016-11594  
; Sequence 11594, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14,755  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11594  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11594

Query Match 72.9%; Score 35; DB 2; Length 361;  
Best Local Similarity 75.0%; Pred. No. 71;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 100 HDIPIGID 107

RESULT 29  
US-09-489-039A-7383  
; Sequence 7383, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 7383  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7383

Query Match 72.9%; Score 35; DB 2; Length 374;  
Best Local Similarity 85.7%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8  
Db 203 DAPAGYD 209

RESULT 30  
US-09-252-991A-26250  
; Sequence 26250, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26250

LENGTH: 490  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26250

Query Match  
Best Local Similarity 72.9%; Score 35; DB 2; Length 490;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGVD 8  
Db 248 HEAPVGLD 255

RESULT 31  
US-09-134-001C-3891  
Sequence 3891, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucelte-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3891  
LENGTH: 649  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3891

Query Match  
Best Local Similarity 72.9%; Score 35; DB 2; Length 649;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIGVD 8  
Db 339 HDLKIIGVD 346

RESULT 32  
US-08-584-226-22  
Sequence 22, Application US/08584226  
Patent No. 5798240  
GENERAL INFORMATION:  
APPLICANT: Martinis, Susan A.  
APPLICANT: Sasansfar, Mandana  
APPLICANT: Kim, Sunghoon  
APPLICANT: Lee, Sang Ho  
APPLICANT: Schimmel, Paul R.  
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL METHIONYL-tRNA  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,226  
FILING DATE:

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/305,766  
FILING DATE: 13-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: CP194-05Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-584-226-22

Query Match  
Best Local Similarity 70.8%; Score 34; DB 1; Length 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGY 7  
Db 5 DAPIGY 10

RESULT 33  
US-09-747-287A-91  
Sequence 91, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
APPLICANT: PACKARD, BEVERLY S.  
TITLE OF INVENTION: HOMO-DOBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: Patent version 3.3  
SEQ ID NO 91  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide.  
US-09-747-287A-91

Query Match  
Best Local Similarity 70.8%; Score 34; DB 2; Length 16;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6  
Db 7 HDAPVG 12

RESULT 34  
US-09-747-287A-92  
Sequence 92, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
APPLICANT: PACKARD, BEVERLY S.



```

; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 92
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-92
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Query Match      70.8%; Score 34; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 HDAPIG 6
Db      7 HDAPVG 12
```

```

RESULT 35
US-09-747-287A-93
; Sequence 93, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-93
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```
Query Match      70.8%; Score 34; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HDAPIG 6
Db      7 HDAPVG 12
```

```

RESULT 36
US-09-747-287A-206
; Sequence 206, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
```

```

; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 206
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287A-206
```

```
Query Match      70.8%; Score 34; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HDAPIG 6
Db      6 HDAPVG 11
```

```

RESULT 37
US-09-747-287A-94
; Sequence 94, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
```

US-09-747-287A-94

Query Match 70.8%; Score 34; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 4.8;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6  
|||:|  
Db 8 HDAPVG 13

RESULT 38

US-09-747-287A-95  
Sequence 95, Application US/09747287A  
Patent No. 6893868

GENERAL INFORMATION:

APPLICANT: KOMORIYA, AKIRA

APPLICANT: PACKARD, BEVERLY S.

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

FILE REFERENCE: 300-948600US

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981

PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882

NUMBER OF SEQ ID NOS: 246

SOFTWARE: PatentIn version 3.3

SEQ ID NO 95

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: Synthetic peptide.

FEATURE: NAME/KEY: misc\_feature

LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

FEATURE: NAME/KEY: misc\_feature

LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

US-09-747-287A-95

Query Match 70.8%; Score 34; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 4.8;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6  
|||:|  
Db 8 HDAPVG 13

RESULT 39

US-09-747-287A-96  
Sequence 96, Application US/09747287A  
Patent No. 6893868

GENERAL INFORMATION:

APPLICANT: KOMORIYA, AKIRA

APPLICANT: PACKARD, BEVERLY S.

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

FILE REFERENCE: 300-948600US

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981

SOFTWARE: PatentIn version 3.3

SEQ ID NO 96

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: Synthetic peptide.

FEATURE: NAME/KEY: misc\_feature

LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

FEATURE: NAME/KEY: misc\_feature

LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

US-09-747-287A-97

PRIOR FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 246

SOFTWARE: PatentIn version 3.3

SEQ ID NO 96

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: Synthetic peptide.

FEATURE: NAME/KEY: misc\_feature

LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

FEATURE: NAME/KEY: misc\_feature

LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

US-09-747-287A-96

Query Match 70.8%; Score 34; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 4.8;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6  
|||:|  
Db 8 HDAPVG 13

RESULT 40

US-09-747-287A-97  
Sequence 97, Application US/09747287A  
Patent No. 6893868

GENERAL INFORMATION:

APPLICANT: KOMORIYA, AKIRA

APPLICANT: PACKARD, BEVERLY S.

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

FILE REFERENCE: 300-948600US

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981

PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882

NUMBER OF SEQ ID NOS: 246

SOFTWARE: PatentIn version 3.3

SEQ ID NO 97

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: Synthetic peptide.

FEATURE: NAME/KEY: misc\_feature

LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

FEATURE: NAME/KEY: misc\_feature

LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

US-09-747-287A-97

Query Match 70.8%; Score 34; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 4.8;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6  
|||:|  
Db 8 HDAPVG 13

Mon Dec 5 15:29:53 2005

us-10-807-553-2.ra1

Page 15

Search completed: December 3, 2005, 23:28:29  
Job time : 25 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 23:28:34 ; Search time 163 Seconds  
(without alignments)  
20.507 Million cell updates/sec

Title: US-10-807-553-2  
Perfect score: 48  
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	8	4	US-10-007-363-2
2	48	100.0	8	4	US-10-807-553-2
3	48	100.0	8	6	US-11-011-557-3
4	48	100.0	30	6	US-11-011-557-93
5	48	100.0	156	3	US-09-771-161A-104
6	48	100.0	737	3	US-09-771-161A-195
7	48	100.0	737	4	US-10-228-931-4
8	48	100.0	737	5	US-10-466-162-2
9	48	100.0	737	5	US-10-756-149-4713
10	44	91.7	8	4	US-10-007-363-7
11	44	91.7	8	4	US-10-007-363-13
12	44	91.7	8	4	US-10-807-553-7
13	44	91.7	8	4	US-10-807-553-13
14	44	91.7	8	6	US-11-011-557-9
15	44	91.7	8	6	US-11-011-557-15
16	44	91.7	8	6	US-11-011-557-31
17	44	89.6	8	4	US-10-007-363-8
18	43	89.6	8	4	US-10-807-553-8
19	43	89.6	8	6	US-11-011-557-10
20	43	89.6	8	6	US-11-011-557-55
21	42	87.5	8	4	US-10-007-363-9
22	42	87.5	8	4	US-10-807-553-9
23	42	87.5	8	6	US-11-011-557-11
24	42	87.5	8	6	US-11-011-557-29
25	40	83.3	8	4	US-10-007-363-12
26	40	83.3	8	4	US-10-007-363-14
27	40	83.3	8	4	US-10-807-553-12

28	40	83.3	8	4	US-10-807-553-14	Sequence 14, Appl
29	40	83.3	8	6	US-11-011-557-14	Sequence 14, Appl
30	40	83.3	8	6	US-11-011-557-16	Sequence 16, Appl
31	40	83.3	8	6	US-11-011-557-21	Sequence 21, Appl
32	40	83.3	8	6	US-11-011-557-79	Sequence 79, Appl
33	39	81.2	586	4	US-10-437-963-131067	Sequence 131067, Appl
34	39	81.2	719	4	US-10-437-963-172827	Sequence 172827, Appl
35	38	79.2	18	6	US-11-011-557-6	Sequence 6, Appl
36	38	79.2	35	4	US-10-199-820-290	Sequence 290, Appl
37	38	79.2	145	4	US-10-424-599-182799	Sequence 182799, Appl
38	38	79.2	682	5	US-10-466-162-4	Sequence 4, Appl
39	38	79.2	683	4	US-10-618-941-72	Sequence 72, Appl
40	38	79.2	683	5	US-10-973-858-40	Sequence 40, Appl
41	38	79.2	8	6	US-11-011-557-67	Sequence 67, Appl
42	37	77.1	171	4	US-10-437-963-123595	Sequence 123595, Appl
43	37	77.1	8	4	US-10-007-363-6	Sequence 6, Appl
44	36	75.0	8	4	US-10-007-363-17	Sequence 17, Appl
45	36	75.0	8	4	US-10-807-553-6	Sequence 6, Appl
46	36	75.0	8	4	US-10-807-553-17	Sequence 17, Appl
47	36	75.0	8	6	US-11-011-557-8	Sequence 8, Appl
48	36	75.0	8	6	US-11-011-557-19	Sequence 19, Appl
49	36	75.0	8	6	US-11-011-557-66	Sequence 66, Appl
50	36	75.0	54	4	US-10-425-115-256425	Sequence 256425, Appl
51	36	75.0	123	4	US-10-425-115-288608	Sequence 288608, Appl
52	36	75.0	396	4	US-10-424-599-276427	Sequence 276427, Appl
53	35	72.9	6	4	US-10-007-363-10	Sequence 10, Appl
54	35	72.9	8	4	US-10-007-363-11	Sequence 11, Appl
55	35	72.9	8	4	US-10-807-553-10	Sequence 10, Appl
56	35	72.9	8	4	US-10-807-553-11	Sequence 11, Appl
57	35	72.9	8	6	US-11-011-557-12	Sequence 12, Appl
58	35	72.9	8	6	US-11-011-557-13	Sequence 13, Appl
59	35	72.9	8	6	US-11-011-557-32	Sequence 32, Appl
60	35	72.9	8	6	US-11-011-557-51	Sequence 51, Appl
61	35	72.9	8	6	US-11-011-557-53	Sequence 53, Appl
62	35	72.9	8	6	US-11-011-557-54	Sequence 54, Appl
63	35	72.9	8	6	US-11-011-557-56	Sequence 56, Appl
64	35	72.9	8	6	US-11-011-557-57	Sequence 57, Appl
65	35	72.9	14	3	US-09-747-287-207	Sequence 207, Appl
66	35	72.9	64	4	US-10-437-963-158408	Sequence 158408, Appl
67	35	72.9	74	4	US-10-425-115-320832	Sequence 320832, Appl
68	35	72.9	154	4	US-10-424-599-241213	Sequence 241213, Appl
69	35	72.9	192	4	US-10-767-701-51923	Sequence 51923, Appl
70	35	72.9	226	4	US-10-282-122A-71421	Sequence 71421, Appl
71	35	72.9	260	4	US-10-156-761-9832	Sequence 9832, Appl
72	35	72.9	287	3	US-09-925-301-1386	Sequence 1386, Appl
73	35	72.9	419	5	US-10-872-198-39	Sequence 39, Appl
74	35	72.9	419	6	US-10-872-197A-39	Sequence 39, Appl
75	35	72.9	449	5	US-10-732-923-9276	Sequence 9276, Appl
76	35	72.9	455	4	US-10-437-963-171839	Sequence 171839, Appl
77	35	72.9	456	5	US-10-732-923-8916	Sequence 8916, Appl
78	35	72.9	456	5	US-10-631-467-1616	Sequence 1616, Appl
79	35	72.9	457	5	US-10-732-923-9090	Sequence 9090, Appl
80	35	72.9	457	5	US-10-732-923-9116	Sequence 9116, Appl
81	35	72.9	457	5	US-10-732-923-9267	Sequence 9267, Appl
82	35	72.9	457	5	US-10-732-923-9268	Sequence 9268, Appl
83	35	72.9	457	5	US-10-732-923-9275	Sequence 9275, Appl
84	35	72.9	457	5	US-10-732-923-9277	Sequence 9277, Appl
85	35	72.9	457	5	US-10-631-467-916	Sequence 916, Appl
86	35	72.9	471	4	US-10-369-493-171847	Sequence 171847, Appl
87	35	72.9	540	4	US-10-437-963-171847	Sequence 171847, Appl
88	35	72.9	644	4	US-10-282-122A-70835	Sequence 70835, Appl
89	35	72.9	644	4	US-10-724-974-6325	Sequence 6325, Appl
90	35	72.9	793	5	US-10-450-763-55956	Sequence 55956, Appl
91	35	72.9	1247	5	US-10-450-763-55345	Sequence 55345, Appl
92	35	72.9	16	3	US-09-747-287-91	Sequence 91, Appl
93	35	72.9	16	3	US-09-747-287-92	Sequence 92, Appl
94	35	72.9	16	3	US-09-747-287-93	Sequence 93, Appl
95	35	72.9	16	3	US-09-747-287-93	Sequence 93, Appl
96	35	72.9	16	3	US-09-747-287-93	Sequence 93, Appl
97	35	72.9	16	3	US-09-747-287-93	Sequence 93, Appl
98	35	72.9	16	3	US-09-747-287-93	Sequence 93, Appl
99	35	72.9	16	3	US-09-747-287-93	Sequence 93, Appl
100	35	72.9	16	3	US-09-747-287-93	Sequence 93, Appl

## ALIGNMENTS

ABM

RESULT 1  
US-10-007-363-2  
Sequence 2, Application US/10007363  
Publication No. US2902016835481  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
TITLE OF INVENTION: Ischemia  
FILE REFERENCE: 58600-8209-US00  
CURRENT APPLICATION NUMBER: US/10/007,363  
CURRENT FILING DATE: 2002-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pseudo-epsilon RACK octapeptide  
US-10-007-363-2

Query Match 100.0%; Score 48; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 2  
US-10-807-553-2  
Sequence 2, Application US/10807553  
Publication No. US20040186055A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
TITLE OF INVENTION: Ischemia  
FILE REFERENCE: 58600-8209-US00  
CURRENT APPLICATION NUMBER: US/10/807,553  
CURRENT FILING DATE: 2004-03-22  
PRIOR APPLICATION NUMBER: US/10/007,363  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pseudo-epsilon RACK octapeptide  
US-10-807-553-2

Query Match 100.0%; Score 48; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 3  
US-11-011-557-3  
Sequence 3, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212-US00  
CURRENT APPLICATION NUMBER: US/11/011,557  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-011-557-3

Query Match 100.0%; Score 48; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 4  
US-11-011-557-93  
Sequence 93, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212-US00  
CURRENT APPLICATION NUMBER: US/11/011,557  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 93  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-011-557-93

Query Match 100.0%; Score 48; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.052; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 1 HDAPIGYD 8  
Db 15 HDAPIGYD 22

RESULT 5  
US-09-771-161A-104  
Sequence 104, Application US/09771161A  
Patent No. US20020110811A1  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/724,676

PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 104  
LENGTH: 156  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-104

Query Match 100.0%; Score 48; DB 3; Length 156;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 6  
US-09-771-161A-195  
Sequence 195, Application US/09771161A  
Patent No. US20020110811A1  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771.161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 195  
LENGTH: 737  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-195

Query Match 100.0%; Score 48; DB 3; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 7  
US-10-228-931-4  
Sequence 4, Application US/10228931  
Publication No. US20030051258A1  
GENERAL INFORMATION:  
APPLICANT: Verma, Ajit K  
APPLICANT: Reddig, Peter J  
APPLICANT: Jansen, Aaron P  
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma  
FILE REFERENCE: 960236.97613  
CURRENT APPLICATION NUMBER: US/10/228.931  
CURRENT FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: US/09/772,647  
PRIOR FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 737  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and  
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence  
US-10-228-931-4

Query Match 100.0%; Score 48; DB 4; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 8  
US-10-466-162-2  
Sequence 2, Application US/10466162  
Publication No. US20050170343A1  
GENERAL INFORMATION:  
APPLICANT: EXELIXIS, INC.  
TITLE OF INVENTION: Modulating Insulin Receptor Signaling  
FILE REFERENCE: EX02-001C-PC  
CURRENT APPLICATION NUMBER: US/10/466.162  
CURRENT FILING DATE: 2003-07-11  
PRIOR APPLICATION NUMBER: US 60/261,335  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,694  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,532  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,361  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,531  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,457  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,226  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,304  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,459  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/261,456  
PRIOR FILING DATE: 2001-01-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 737  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-466-162-2

Query Match 100.0%; Score 48; DB 5; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 9  
US-10-756-149-4713  
Sequence 4713, Application US/10756149  
Publication No. US20050181375A1  
GENERAL INFORMATION:  
APPLICANT: Azizi, Natasha  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND  
METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER  
FILE REFERENCE: file  
CURRENT APPLICATION NUMBER: US/10/756.149

CURRENT FILING DATE: 2004-01-12  
NUMBER OF SEQ ID NOS: 5818  
SOFTWARE: Patent version 3.2  
SEQ ID NO 4713  
LENGTH: 737  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-756-149-4713

Query Match 100.0%; Score 48; DB 5; Length 737;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 10  
US-10-007-363-7  
Sequence 7, Application US/10007363  
Publication No. US20020168354A1  
GENERAL INFORMATION:

ABN

APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
FILE REFERENCE: 58600-8209.US00  
CURRENT FILING DATE: 2002-11-09  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-007-363-7

Query Match 91.7%; Score 44; DB 4; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 11  
US-10-007-363-13  
Sequence 13, Application US/10007363  
Publication No. US20020168354A1  
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
FILE REFERENCE: 58600-8209.US00  
CURRENT FILING DATE: 2002-11-09  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide

US-10-007-363-13

Query Match 91.7%; Score 44; DB 4; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 12  
US-10-807-553-7  
Sequence 7, Application US/10807553  
Publication No. US20040186055A1  
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
FILE REFERENCE: 58600-8209.US00  
CURRENT FILING DATE: 2004-03-22  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US/10/007,363  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-807-553-7

Query Match 91.7%; Score 44; DB 4; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 13  
US-10-807-553-13  
Sequence 13, Application US/10807553  
Publication No. US20040186055A1  
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
FILE REFERENCE: 58600-8209.US00  
CURRENT FILING DATE: 2004-03-22  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US/10/007,363  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-807-553-13

Query Match 91.7%; Score 44; DB 4; Length 8;

QY 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 13  
US-10-807-553-13  
Sequence 13, Application US/10807553  
Publication No. US20040186055A1  
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
FILE REFERENCE: 58600-8209.US00  
CURRENT FILING DATE: 2004-03-22  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US/10/007,363  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-807-553-13

Query Match 91.7%; Score 44; DB 4; Length 8;



Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDGPIGYD 8

NO  
C/S  
X  
inv

RESULT 14  
US-11-011-557-9  
Sequence 9, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212.US00  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: US/11/011,557  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 9  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide  
US-11-011-557-9

Query Match 91.7%; Score 44; DB 6; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPIGYE 8

RESULT 15  
US-11-011-557-15  
Sequence 15, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212.US00  
CURRENT APPLICATION NUMBER: US/11/011,557  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 15  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide  
US-11-011-557-15

Query Match 91.7%; Score 44; DB 6; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDGPIGYD 8

RESULT 16

US-11-011-557-31  
Sequence 31, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212.US00  
CURRENT APPLICATION NUMBER: US/11/011,557  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 31  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Alternative pseudo-eta RACK peptide  
US-11-011-557-31

Query Match 91.7%; Score 44; DB 6; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDTPIGYD 8

RESULT 17  
US-10-007-363-8  
Sequence 8, Application US/10007363  
Publication No. US20020168354A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
FILE REFERENCE: 58600-8209.US00  
CURRENT APPLICATION NUMBER: US/10/007,363  
CURRENT FILING DATE: 2002-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-007-363-8

Query Match 89.6%; Score 43; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPVGYE 8

RESULT 18  
US-10-807-553-8  
Sequence 8, Application US/10807553  
Publication No. US20040186055A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
ISCHEMIA

FILE REFERENCE: 58600-8209.US00  
CURRENT APPLICATION NUMBER: US/10/807,553  
CURRENT FILING DATE: 2004-03-22  
PRIOR APPLICATION NUMBER: US/10/007,363  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-807-553-8

Query Match 89.6%; Score 43; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPVGYE 8

RESULT 19  
US-11-011-557-10  
Sequence 10, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212.US00  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 10  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide  
US-11-011-557-10

Query Match 89.6%; Score 43; DB 6; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPVGYE 8

RESULT 20  
US-11-011-557-55  
Sequence 55, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212.US00  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3

SEQ ID NO 55  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: A modification of SEQ ID NO:3  
US-11-011-557-55

Query Match 89.6%; Score 43; DB 6; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HNAPIGYD 8

RESULT 21  
US-10-007-363-9  
Sequence 9, Application US/10007363  
Publication No. US20020168354A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
TITLE OF INVENTION: Ischemia  
FILE REFERENCE: 58600-8209.US00  
CURRENT APPLICATION NUMBER: US/10/007,363  
CURRENT FILING DATE: 2002-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-007-363-9

Query Match 87.5%; Score 42; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPVGYE 8

RESULT 22  
US-10-807-553-9  
Sequence 9, Application US/10807553  
Publication No. US20040186055A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
TITLE OF INVENTION: Ischemia  
FILE REFERENCE: 58600-8209.US00  
CURRENT APPLICATION NUMBER: US/10/807,553  
CURRENT FILING DATE: 2004-03-22  
PRIOR APPLICATION NUMBER: US/10/007,363  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-807-553-9

Query Match 87.5%; Score 42; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPLGYE 8

RESULT 23

US-11-011-557-11  
Sequence 11, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Chen, Leon E.  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212 US00  
CURRENT APPLICATION NUMBER: US/11/011,557  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 11  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide  
US-11-011-557-11

Query Match 87.5%; Score 42; DB 6; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPLGYE 8

RESULT 24

US-11-011-557-29  
Sequence 29, Application US/11011557  
Publication No. US20050187156A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Chen, Leon E.  
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
FILE REFERENCE: 58600-8212 US00  
CURRENT APPLICATION NUMBER: US/11/011,557  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,223  
PRIOR FILING DATE: 2003-12-11  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 29  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Alternative pseudo-eta RACK peptide  
US-11-011-557-29

Query Match 87.5%; Score 42; DB 6; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPLGYE 8

Db 1 HDAPLGYD 8

RESULT 25  
US-10-007-363-12  
Sequence 12, Application US/10007363  
Publication No. US20020168354A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to Ischemia  
FILE REFERENCE: 58600-8209 US00  
CURRENT APPLICATION NUMBER: US/10/007,363  
CURRENT FILING DATE: 2002-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-007-363-12

Query Match 83.3%; Score 40; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
Db 2 DAPIGYD 8

RESULT 26

US-10-007-363-14  
Sequence 14, Application US/10007363  
Publication No. US20020168354A1  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to Ischemia  
FILE REFERENCE: 58600-8209 US00  
CURRENT APPLICATION NUMBER: US/10/007,363  
CURRENT FILING DATE: 2002-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified pseudo-epsilon RACK peptide  
US-10-007-363-14

Query Match 83.3%; Score 40; DB 4; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 1 HDAPLGYD 8

RESULT 27  
US-10-807-553-12  
Sequence 12, Application US/10807553  
Publication No. US20040186055A1

```
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209.US00
; CURRENT APPLICATION NUMBER: US/10/807,553
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US/10/007,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-12
```

```
Query Match      83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
        |||||
Db       2 DAPIGYD 8
```

```
RESULT 28
US-10-807-553-14
; Sequence 14, Application US/10807553
; Publication No. US20040186055A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209.US00
; CURRENT APPLICATION NUMBER: US/10/807,553
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US/10/007,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-14
```

```
Query Match      83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 HDAPIGYD 8
        |||||
Db       1 HDAPIGYD 8
```

```
RESULT 29
US-11-011-557-14
; Sequence 14, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Chen, Leon E.
```

```
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-14
```

```
Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
        |||||
Db       2 DAPIGYD 8
```

```
RESULT 30
US-11-011-557-16
; Sequence 16, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-16
```

```
Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 HDAPIGYD 8
        |||||
Db       1 HDAPIGYD 8
```

```
RESULT 31
US-11-011-557-21
; Sequence 21, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
```

```

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-21

```

```

Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 HDAPIGYD 8
        |||||
Db      1 HDAPIDPYD 8

```

```

RESULT 32
US-11-011-557-79
; Sequence 79, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; PRIORITY FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-79

```

```

Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 HDAPIGYD 8
        |||||
Db      1 HDAPIDPYD 8

```

```

RESULT 33
US-10-437-963-131067
; Sequence 131067, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barzak, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIORITY FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 131067
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_33169C.1.pep

```

```

US-10-437-963-131067

```

```

Query Match      81.2%; Score 39; DB 4; Length 586;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 HDAPIGYD 8
        |||||
Db      408 HDVPIGHD 415

```

```

RESULT 34
US-10-437-963-172827
; Sequence 172827, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barzak, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIORITY FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172827
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70925C.1.pep
US-10-437-963-172827

```

```

Query Match      81.2%; Score 39; DB 4; Length 719;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 DAPIGYD 8
        |||||
Db      553 DAPVGYD 559

```

```

RESULT 35
US-11-011-557-6
; Sequence 6, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; PRIORITY FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-011-557-6

```

```

Query Match      79.2%; Score 38; DB 6; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 HDAPIGYD 8

```

Db 1 HETPLGYD 8

RESULT 36  
US-11-011-557-96  
; Sequence 96, Application US/11011557  
; Publication No. US20050187156A1  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Chen, Leon E.  
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
; FILE REFERENCE: 58600-8212.US00  
; CURRENT APPLICATION NUMBER: US/11/011,557  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: 60/529,223  
; PRIOR FILING DATE: 2003-12-11  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 96  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-011-557-96

Query Match 79.2% Score 38; DB 6; Length 18;  
Best Local Similarity 62.5% Pred. No. 2.6;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
||:||||  
Db 6 HETPLGYD 13

RESULT 37  
US-10-199-820-290  
; Sequence 290, Application US/10199820  
; Publication No. US20030180739A1  
; GENERAL INFORMATION:  
; APPLICANT: Board of Trustees of the University of Illinois  
; APPLICANT: Primianno, Thomas  
; APPLICANT: Chang, Bey-din  
; APPLICANT: Robinson, Igor  
; TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating Ca  
; FILE REFERENCE: 99,216-U  
; CURRENT APPLICATION NUMBER: US/10/199,820  
; CURRENT FILING DATE: 2002-09-23  
; NUMBER OF SEQ ID NOS: 314  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 290  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-199-820-290

Query Match 79.2% Score 38; DB 4; Length 35;  
Best Local Similarity 62.5% Pred. No. 5.2;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
||:||||  
Db 16 HETPLGYD 23

RESULT 38  
US-10-424-599-182799  
; Sequence 182799, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 182799  
; LENGTH: 145  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURES:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_136081C.1.pep  
US-10-424-599-182799

Query Match 79.2% Score 38; DB 4; Length 145;  
Best Local Similarity 71.4% Pred. No. 23;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGY 7  
||:||||  
Db 4 HDSPVGY 10

RESULT 39  
US-10-466-162-4  
; Sequence 4, Application US/10466162  
; Publication No. US20050170343A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling  
; FILE REFERENCE: EX02-001C-PC  
; CURRENT APPLICATION NUMBER: US/10/466,162  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: US 60/261,335  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,694  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,532  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,361  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,531  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,457  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,226  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,304  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,459  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,456  
; PRIOR FILING DATE: 2001-01-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 682  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-466-162-4

Query Match 79.2% Score 38; DB 5; Length 682;  
Best Local Similarity 62.5% Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
||:||||  
Db 88 HETPLGYD 95

RESULT 40  
US-10-618-941-72

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; Sequence 72, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-618-941-72
```

```
Query Match 79.2%; Score 38; DB 4; Length 683;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 HDAPIGYD 8
|:|:|
Db 88 HETPLGYD 95
```

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Search completed: December 3, 2005, 23:45:38
Job time : 165 secs
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November 2005

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Published\_Application Nucleic Acid and Published\_Application Amino Acid database searches now generate two sets of results each. The Published\_Application databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Application\_New databases; older published applications make up the Published\_Application\_Main databases.

Searches run against Nucleic Acid Published\_Application produce two sets of results, with the extensions **.rnpbm** (Published\_Application\_NA\_Main) and **.rnpbn** (Published\_Application\_NA\_New).

Searches run against Amino Acid Published\_Application produce two sets of results, with the extensions **.rapbm** (Published\_Application\_AA\_Main) and **.rapbn** (Published\_Application\_AA\_New).

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## OM protein - protein search, using sw model1

Run on: December 3, 2005, 23:29:20 ; Search time 11 Seconds  
(without alignments)  
3.482 Million cell updates/sec

Title: US-10-807-553-2  
Perfect score: 48  
Sequence: 1 HDAPICVD 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

## Database :

Published Applications AA New:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/PCRT\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US00\_NEW\_PUB.pep:\*

\*Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	70.8	485	6	US-10-467-657-2498
2	33	68.8	164	6	US-10-467-657-2912
3	33	68.8	719	6	US-10-467-657-762
4	32	66.7	102	6	US-10-816-768-45
5	32	66.7	595	6	US-10-510-386-240
6	31	64.6	496	7	US-11-067-121-3
7	30	62.5	496	7	US-11-067-121-12
8	30	62.5	659	6	US-10-467-657-6006
9	29.5	61.5	199	6	US-10-467-657-2460
10	29	60.4	150	7	US-11-074-176-102
11	29	60.4	417	6	US-10-971-560-4
12	29	60.4	494	6	US-10-971-560-7
13	29	60.4	501	6	US-10-971-560-2
14	29	60.4	501	6	US-10-971-560-10
15	29	60.4	501	6	US-11-067-121-1
16	29	60.4	530	6	US-10-980-388-62
17	28	58.3	284	7	US-11-055-822-692
18	28	58.3	284	7	US-11-055-822-770
19	28	58.3	310	6	US-10-467-657-7412
20	28	58.3	326	6	US-10-793-626-254
21	28	58.3	480	6	US-10-510-386-12
22	28	58.3	674	6	US-10-467-657-6812
23	27.5	57.3	433	6	US-10-667-295-83
24	27.5	57.3	434	6	US-10-667-295-141
25	27.5	57.3	505	6	US-10-667-295-82

26	27.5	57.3	506	6	US-10-667-295-140	Sequence 140, App
27	27.5	57.3	526	6	US-10-667-295-139	Sequence 139, App
28	27.5	57.3	534	6	US-10-667-295-81	Sequence 81, Appl
29	27	56.2	54	6	US-10-467-657-412	Sequence 412, App
30	27	56.2	92	6	US-10-467-657-3158	Sequence 3158, App
31	27	56.2	405	6	US-10-467-657-2310	Sequence 2310, Ap
32	27	56.2	413	6	US-10-467-657-1858	Sequence 1858, Ap
33	27	56.2	435	6	US-10-467-657-4570	Sequence 4570, Ap
34	27	56.2	443	6	US-10-793-626-1200	Sequence 1200, Ap
35	27	56.2	528	6	US-10-467-657-6146	Sequence 6146, Ap
36	27	56.2	534	6	US-10-467-657-468	Sequence 468, App
37	27	56.2	611	7	US-11-082-389-436	Sequence 436, App
38	27	56.2	680	6	US-10-467-657-2008	Sequence 2008, Ap
39	27	56.2	756	6	US-10-467-657-8694	Sequence 8694, Ap
40	27	56.2	872	6	US-10-467-657-78	Sequence 78, Appl
41	27	56.2	886	6	US-10-467-657-4544	Sequence 4544, Ap
42	27	56.2	1388	6	US-10-821-334-1143	Sequence 1143, Ap
43	27	56.2	1560	7	US-11-059-982-1	Sequence 1, Appl1
44	26	54.2	18	6	US-10-416-384-12	Sequence 12, Appl
45	26	54.2	148	6	US-10-512-109-12	Sequence 19, Appl
46	26	54.2	148	6	US-10-512-109-21	Sequence 8302, Ap
47	26	54.2	182	6	US-10-467-657-8302	Sequence 11, Appl
48	26	54.2	185	7	US-11-132-839-11	Sequence 11, Appl
49	26	54.2	203	7	US-11-132-839-10	Sequence 12, Appl
50	26	54.2	211	7	US-11-132-839-12	Sequence 21, Appl
51	26	54.2	228	6	US-10-848-689-1	Sequence 1, Appl1
52	26	54.2	243	6	US-10-131-826A-362	Sequence 362, App
53	26	54.2	243	6	US-10-512-109-23	Sequence 23, Appl
54	26	54.2	243	6	US-10-512-109-48	Sequence 48, Appl
55	26	54.2	244	6	US-10-793-626-994	Sequence 994, App
56	26	54.2	245	6	US-10-793-626-2916	Sequence 2916, Ap
57	26	54.2	248	6	US-11-082-389-436	Sequence 438, App
58	26	54.2	282	6	US-10-467-657-5450	Sequence 5450, Ap
59	26	54.2	280	7	US-11-054-515-3231	Sequence 3231, Ap
60	26	54.2	282	6	US-10-467-657-5564	Sequence 5564, Ap
61	26	54.2	306	7	US-11-017-550-43	Sequence 43, Appl
62	26	54.2	309	7	US-11-065-669-2	Sequence 2, Appl1
63	26	54.2	309	7	US-11-054-515-3230	Sequence 3230, Ap
64	26	54.2	341	6	US-10-821-334-1628	Sequence 1628, Ap
65	26	54.2	352	7	US-11-108-528-20	Sequence 20, Appl
66	26	54.2	352	7	US-11-108-528-22	Sequence 22, Appl
67	26	54.2	360	6	US-10-793-626-2150	Sequence 2150, Ap
68	26	54.2	376	6	US-10-793-626-2106	Sequence 2106, Ap
69	26	54.2	386	7	US-11-055-822-586	Sequence 586, App
70	26	54.2	489	6	US-10-467-657-2096	Sequence 2096, App
71	26	54.2	500	6	US-10-467-657-594	Sequence 594, App
72	26	54.2	552	7	US-11-074-176-204	Sequence 204, App
73	26	54.2	552	7	US-10-467-657-4826	Sequence 4826, Ap
74	26	54.2	589	6	US-10-467-657-3802	Sequence 3802, Ap
75	26	54.2	687	6	US-10-485-517-274	Sequence 274, App
76	26	54.2	720	7	US-11-102-240-38	Sequence 38, Appl
77	26	54.2	725	6	US-10-467-657-1536	Sequence 1536, Ap
78	26	54.2	747	7	US-11-182-592-2	Sequence 2, Appl1
79	26	54.2	787	6	US-10-467-657-2832	Sequence 2832, Ap
80	26	54.2	835	6	US-10-501-039-4	Sequence 4, Appl1
81	26	54.2	865	6	US-10-467-657-33	Sequence 33, Appl
82	26	54.2	1238	7	US-11-078-735-21	Sequence 21, Appl
83	26	54.2	1432	6	US-10-510-386-218	Sequence 218, App
84	26	54.2	1437	7	US-11-074-176-96	Sequence 96, Appl
85	26	54.2	1437	7	US-11-055-822-24	Sequence 24, Appl
86	25.5	53.1	20	7	US-11-054-515-2500	Sequence 2500, Ap
87	25	52.1	21	6	US-10-939-890-526	Sequence 526, App
88	25	52.1	21	6	US-10-939-890-578	Sequence 578, App
89	25	52.1	21	6	US-10-821-334-1132	Sequence 1132, App
90	25	52.1	94	7	US-11-055-822-86	Sequence 86, Appl
91	25	52.1	124	6	US-10-467-657-1132	Sequence 1132, Ap
92	25	52.1	143	6	US-10-793-626-1182	Sequence 1182, App
93	25	52.1	143	6	US-10-793-626-1940	Sequence 1940, Ap
94	25	52.1	143	6	US-10-467-657-2862	Sequence 2862, Ap
95	25	52.1	149	6	US-10-957-569-38	Sequence 38, Appl
96	25	52.1	152	6	US-10-467-657-8825	Sequence 8825, Ap
97	25	52.1	183	6	US-10-467-657-8825	Sequence 8825, Ap
98	25	52.1	183	7	US-11-055-822-84	Sequence 84, Appl

99 25 52.1 252 7 US-11-054-515-1416 Sequence 1416, App  
100 25 52.1 287 7 US-11-055-822-102 Sequence 102, App

## ALIGNMENTS

## RESULT 1

US-10-467-657-2498  
; Sequence 2498, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 2498  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2498

Query Match 70.8%; Score 34; DB 6; Length 485;  
Best Local Similarity 85.7%; Pred. No. 5.6;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGY 7  
|||

DB 226 HDASIGY 232

## RESULT 2

US-10-467-657-2912  
; Sequence 2912, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 2912  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2912

Query Match 68.8%; Score 33; DB 6; Length 164;  
Best Local Similarity 83.3%; Pred. No. 2.8;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APIGYD 8  
|||

DB 47 APIGYD 52

RESULT 3  
US-10-467-657-762  
; Sequence 762, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 762  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-762

Query Match 68.8%; Score 33; DB 6; Length 719;  
Best Local Similarity 83.3%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGY 7  
|||

DB 299 DAPIGY 304

## RESULT 4

US-10-816-768-45  
; Sequence 45, Application US/10816768  
; Publication No. US20050250936A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STR-075  
; CURRENT APPLICATION NUMBER: US/10/816,768  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 45  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: DPP  
US-10-816-768-45

Query Match 66.7%; Score 32; DB 6; Length 102;  
Best Local Similarity 83.3%; Pred. No. 2.6;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APIGYD 8  
|||

DB 21 APIGYD 26

## RESULT 5

US-10-510-386-240  
; Sequence 240, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Olsen, Peter Bjarke

APPLICANT: Rasmussen, Michael Dolberg  
TITLE OF INVENTION: Improved Bacillus Host Cell  
FILE REFERENCE: 10294-204-US  
CURRENT APPLICATION NUMBER: US/10/510,386  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 248  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 240  
LENGTH: 595  
TYPE: PRT  
ORGANISM: Bacillus licheniformis  
US-10-510-386-240

Query Match 66.7%; Score 32; DB 6; Length 595;  
Best Local Similarity 62.5%; Pred. No. 18;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 284 HNAFLPYD 291

RESULT 6  
US-11-067-121-3  
Sequence 3, Application US/11067121  
Publication No. US20050261185A1  
GENERAL INFORMATION:  
APPLICANT: Martijn, Cecile  
APPLICANT: Rondahl, Lena  
TITLE OF INVENTION: THERAPEUTIC PROTEINS  
FILE REFERENCE: 18909-002001  
CURRENT APPLICATION NUMBER: US/11/067,121  
CURRENT FILING DATE: 2005-02-25  
PRIOR APPLICATION NUMBER: US 60/576,445  
PRIOR FILING DATE: 2004-06-02  
PRIOR APPLICATION NUMBER: SE 0400489-1  
PRIOR FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Mus musculus  
US-11-067-121-3

Query Match 64.6%; Score 31; DB 7; Length 496;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
Db 68 DAPIDYD 74

RESULT 7  
US-11-067-121-12  
Sequence 12, Application US/11067121  
Publication No. US20050261185A1  
GENERAL INFORMATION:  
APPLICANT: Martijn, Cecile  
APPLICANT: Rondahl, Lena  
TITLE OF INVENTION: THERAPEUTIC PROTEINS  
FILE REFERENCE: 18909-002001  
CURRENT APPLICATION NUMBER: US/11/067,121  
CURRENT FILING DATE: 2005-02-25  
PRIOR APPLICATION NUMBER: US 60/576,445  
PRIOR FILING DATE: 2004-06-02  
PRIOR APPLICATION NUMBER: SE 0400489-1  
PRIOR FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 496

TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-067-121-12

Query Match 62.5%; Score 30; DB 7; Length 496;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
Db 68 DAPIDYD 74

RESULT 8  
US-10-467-657-6006  
Sequence 6006, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 6006  
LENGTH: 659  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6006

Query Match 62.5%; Score 30; DB 6; Length 659;  
Best Local Similarity 62.5%; Pred. No. 50;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
Db 258 HGAPLGAD 265

RESULT 9  
US-10-467-657-2460  
Sequence 2460, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 2460  
LENGTH: 199  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2460

Query Match 61.5%; Score 29.5; DB 6; Length 199;  
Best Local Similarity 46.2%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

OY 1 HDAP1-----GYD 8  
|||  
Db 148 HDTPLGQNGFGYD 160

RESULT 10  
US-11-074-176-102  
; Sequence 102, Application US/11074176  
; Publication No. US20050250135A1  
; GENERAL INFORMATION:  
; APPLICANT: Kjaerhammer, Todd R.  
; APPLICANT: Russell, William M.  
; APPLICANT: Altermann, Eric  
; APPLICANT: McCalliffe, Olivia  
; APPLICANT: Perill, Andrea Azcarate  
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding  
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore  
; FILE REFERENCE: 5051-694  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR FILING DATE: 2004-03-08  
; PRIOR FILING DATE: 2004-03-08  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 102  
; LENGTH: 150  
; TYPE: PRT  
; ORGANISM: Lactobacillus acidophilus  
US-11-074-176-102

Query Match 60.4%; Score 29; DB 7; Length 150;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAP1 5  
|||||  
Db 140 HDAP1 144

RESULT 11  
US-10-971-560-4  
; Sequence 4, Application US/10971560  
; Publication No. US20050244842A1  
; GENERAL INFORMATION:  
; APPLICANT: Enerbck, Sven  
; APPLICANT: Krook, Katarina  
; APPLICANT: Rondahl, Lena  
; APPLICANT: Wasserman, Weth  
; TITLE OF INVENTION: PROMOTER SEQUENCES  
; FILE REFERENCE: 13425-042001  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR FILING DATE: 2004-09-26  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-971-560-4

Query Match 60.4%; Score 29; DB 6; Length 417;  
Best Local Similarity 62.5%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 HDAP1GYD 8  
|||  
Db 406 HAAFYSD 413

RESULT 12  
US-10-971-560-7  
; Sequence 7, Application US/10971560  
; Publication No. US20050244842A1  
; GENERAL INFORMATION:  
; APPLICANT: Enerbck, Sven  
; APPLICANT: Krook, Katarina  
; APPLICANT: Rondahl, Lena  
; APPLICANT: Wasserman, Weth  
; TITLE OF INVENTION: PROMOTER SEQUENCES  
; FILE REFERENCE: 13425-042001  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR FILING DATE: 2004-09-26  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-971-560-7

Query Match 60.4%; Score 29; DB 6; Length 494;  
Best Local Similarity 62.5%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 HDAP1GYD 8  
|||  
Db 483 HAAFYSD 490

RESULT 13  
US-10-971-560-2  
; Sequence 2, Application US/10971560  
; Publication No. US20050244842A1  
; GENERAL INFORMATION:  
; APPLICANT: Enerbck, Sven  
; APPLICANT: Krook, Katarina  
; APPLICANT: Rondahl, Lena  
; APPLICANT: Wasserman, Weth  
; TITLE OF INVENTION: PROMOTER SEQUENCES  
; FILE REFERENCE: 13425-042001  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR FILING DATE: 2004-09-26  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-971-560-2

Query Match 60.4%; Score 29; DB 6; Length 501;

Best Local Similarity 62.5%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 490 HAAPYSYD 497

## RESULT 14

US-10-971-560-10  
; Sequence 10, Application US/10971560  
; Publication No. US20050244842A1  
; GENERAL INFORMATION:  
; APPLICANT: Enerbck, Sven  
; APPLICANT: Krook, Katarina  
; APPLICANT: Rondahl, Lena  
; APPLICANT: Wasserman, Wyeth  
; TITLE OF INVENTION: PROMOTER SEQUENCES  
; FILE REFERENCE: 13425-042001  
; CURRENT APPLICATION NUMBER: US/10/971,560  
; PRIOR FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: US/09/963,285  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: SE 0004102-0  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/238,897  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: SE 0003435-5  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-971-560-10

Query Match 60.4%; Score 29; DB 6; Length 501;  
Best Local Similarity 62.5%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 490 HAAPYSYD 497

## RESULT 15

US-11-067-121-1  
; Sequence 1, Application US/11067121  
; Publication No. US2005026185A1  
; GENERAL INFORMATION:  
; APPLICANT: Martijn, Cecile  
; APPLICANT: Rondahl, Lena  
; TITLE OF INVENTION: THERAPEUTIC PROTEINS  
; FILE REFERENCE: 18909-002001  
; CURRENT APPLICATION NUMBER: US/11/067,121  
; PRIOR FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: US 60/576,445  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: SE 0400489-1  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-067-121-1

Query Match 60.4%; Score 29; DB 7; Length 501;  
Best Local Similarity 62.5%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 490 HAAPYSYD 497

## RESULT 16

US-10-980-388-62  
; Sequence 62, Application US/10980388  
; Publication No. US20050255490A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Hiesch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kayes, Paul S.  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl.  
; FILE REFERENCE: 00325 US1  
; CURRENT APPLICATION NUMBER: US/10/980,388  
; PRIOR FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/09/791,932  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,304  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,303  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,397  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,247  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/188,880  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/217,369  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/217,370  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/218,492  
; PRIOR FILING DATE: 2000-07-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 62  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-980-388-62

Query Match 60.4%; Score 29; DB 6; Length 530;  
Best Local Similarity 66.7%; Pred. No. 63;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6  
Db 521 HEAPLG 526

## RESULT 17

US-11-055-822-692  
; Sequence 692, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Krogger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Heberhauser, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; FILE REFERENCE: BGI-121CPCN

```
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 692
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-692
```

```
Query Match          58.3%; Score 28; DB 7; Length 284;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGVD 8
        |||||
Db      261 HDVPSRD 268
```

```
RESULT 18
US-11-055-822-770
; Sequence 770, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroege, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habermann, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121PCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
```

```
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 770
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-770
```

```
Query Match          58.3%; Score 28; DB 7; Length 284;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGVD 8
        |||||
Db      261 HDVPSRD 268
```

```
RESULT 19
US-10-467-657-7412
; Sequence 7412, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7412
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7412
```

```
Query Match          58.3%; Score 28; DB 6; Length 310;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGV 7
        |||||
Db      3 HIPPIGV 9
```

```
RESULT 20
US-10-793-626-254
; Sequence 254, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 254
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-254
```



Query Match 58.3%; Score 28; DB 6; Length 326;  
Best Local Similarity 83.3%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGY 7  
Db 187 DFIGY 192

RESULT 21  
US-10-510-386-12  
; Sequence 12, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Olsen, Peter Bjarke  
; APPLICANT: Rasmussen, Michael Dolberg  
; TITLE OF INVENTION: Improved Bacillus Host Cell  
; FILE REFERENCE: 10294.204-US  
; CURRENT APPLICATION NUMBER: US/10/510.386  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn Version 3.3  
; SEQ ID NO 12  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Bacillus licheniformis  
US-10-510-386-12

Query Match 58.3%; Score 28; DB 6; Length 480;  
Best Local Similarity 66.7%; Pred. No. 90;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGY 7  
Db 210 DKPGY 215

RESULT 22  
US-10-467-657-812  
; Sequence 6812, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIIGNI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467.657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6812  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-812

Query Match 58.3%; Score 28; DB 6; Length 674;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPGY 7  
Db 111 HDKRGY 117

RESULT 23  
US-10-667-295-83  
; Sequence 83, Application US/10667295  
; Publication No. US20050257293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter  
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM  
; FILE REFERENCE: 11696-047001  
; CURRENT APPLICATION NUMBER: US/10/667.295  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: US 60/411.823  
; PRIOR FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 263  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 433  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(433)  
; OTHER INFORMATION: Ceres Seq. ID no. 12558792  
US-10-667-295-83

Query Match 57.3%; Score 27.5; DB 6; Length 433;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HDAPGY 8  
Db 309 HDKRGY 317

RESULT 24  
US-10-667-295-141  
; Sequence 141, Application US/10667295  
; Publication No. US20050257293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter  
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM  
; FILE REFERENCE: 11696-047001  
; CURRENT APPLICATION NUMBER: US/10/667.295  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: US 60/411.823  
; PRIOR FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 263  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 141  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(434)  
; OTHER INFORMATION: Ceres Seq. ID no. 13531808  
US-10-667-295-141

Query Match 57.3%; Score 27.5; DB 6; Length 434;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HDAPGY 8  
Db 310 HDKRGY 318

RESULT 25  
US-10-667-295-82  
; Sequence 82, Application US/10667295  
; Publication No. US20050257293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter

```
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 82
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(505)
; OTHER INFORMATION: Ceres Seq. ID no. 12558791
US-10-667-295-82
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 505;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      381 HDAKLAGYD 389
```

```
RESULT 26
US-10-667-295-140
; Sequence 140, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 140
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(506)
; OTHER INFORMATION: Ceres Seq. ID no. 13531807
US-10-667-295-140
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 506;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      382 HDAKLAGYD 390
```

```
RESULT 27
US-10-667-295-139
; Sequence 139, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 139
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(526)
; OTHER INFORMATION: Ceres Seq. ID no. 13531806
US-10-667-295-139
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 526;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      402 HDAKLAGYD 410
```

```
RESULT 28
US-10-667-295-81
; Sequence 81, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 81
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(534)
; OTHER INFORMATION: Ceres Seq. ID no. 12558790
US-10-667-295-81
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 534;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      410 HDAKLAGYD 418
```

```
RESULT 29
US-10-467-657-412
; Sequence 412, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 412
; LENGTH: 54
```

TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-412

Query Match 56.2%; Score 27; DB 6; Length 54;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 6  
Db 2 HDSBAG 7

RESULT 30  
US-10-467-657-3158

Sequence 3158, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
PRIOR FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 3158  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3158

Query Match 56.2%; Score 27; DB 6; Length 92;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 6  
Db 46 HSAPIG 51

RESULT 31  
US-10-467-657-2310

Sequence 2310, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
PRIOR FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 2310  
LENGTH: 405  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2310

Query Match 56.2%; Score 27; DB 6; Length 405;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APICVD 8  
Db 103 APDGYD 108

RESULT 32  
US-10-467-657-1858

Sequence 1858, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
PRIOR FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 1858  
LENGTH: 413  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1858

Query Match 56.2%; Score 27; DB 6; Length 413;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 6  
Db 155 HHAPVG 160

RESULT 33  
US-10-467-657-4570

Sequence 4570, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
PRIOR FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 4570  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4570

Query Match 56.2%; Score 27; DB 6; Length 435;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 7  
Db 258 HDAVLGF 264

RESULT 34

US-10-793-626-1200  
; Sequence 1200, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PUS480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: SeqMan9, version 1.04  
; SEQ ID NO 1200  
; LENGTH: 443  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-1200

Query Match 56.2%; Score 27; DB 6; Length 443;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
|:|  
|:|  
Db 49 DLPVDYD 55

RESULT 35  
US-10-467-657-6146  
; Sequence 6146, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqMan9, version 1.04  
; SEQ ID NO 6146  
; LENGTH: 528  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6146

Query Match 56.2%; Score 27; DB 6; Length 528;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 7  
|:|  
|:|  
Db 353 DEPIGYD 358

RESULT 36  
US-10-467-657-468  
; Sequence 468, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqMan9, version 1.04  
; SEQ ID NO 468  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-468

Query Match 56.2%; Score 27; DB 6; Length 544;  
Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
|:|  
|:|  
Db 127 HEGMAGYD 134

RESULT 37  
US-11-082-389-436  
; Sequence 436, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompeius, Markus  
; APPLICANT: Kroeger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauser, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; FILE REFERENCE: BG1-131CPCN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 436  
; LENGTH: 611  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-082-389-436

Query Match 56.2%; Score 27; DB 7; Length 611;  
Best Local Similarity 57.1%; Pred. No. 1.9e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DAPIGYD 8

Db 148 DGPVEYD 154

## RESULT 38

US-10-467-657-2008  
; Sequence 2008, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2008  
; LENGTH: 680  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2008

## Query Match

Best Local Similarity 56.2%; Score 27; DB 6; Length 680;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIG 6

Db 50 DAPIG 54

## RESULT 39

US-10-467-657-8694  
; Sequence 8694, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8694  
; LENGTH: 756  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8694

## Query Match

Best Local Similarity 56.2%; Score 27; DB 6; Length 756;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 APIGYD 8

Db 541 SPIGPD 546

## RESULT 40

US-10-467-657-78  
; Sequence 78, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 78  
; LENGTH: 872  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-78

## Query Match

Best Local Similarity 56.2%; Score 27; DB 6; Length 872;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8

Db 674 NDFRIGYD 681

Search completed: December 3, 2005, 23:45:54  
Job time : 12 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 23:23:38 / Search time 37 Seconds  
(without alignments)  
20.804 Million cell updates/sec

Title: US-10-807-553-2  
Perfect score: 48  
Sequence: 1 HDAPIGYD 8

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	736	1	KIRBCE
2	48	100.0	737	1	KIRSCB
3	48	100.0	737	1	KIRSCB
4	48	100.0	737	1	KIRSCB
5	39	81.2	652	2	T39409
6	39	81.2	869	1	UC4858
7	38	79.2	682	1	A39666
8	38	79.2	683	1	A23690
9	38	79.2	683	1	S29478
10	38	79.2	1025	2	T10259
11	37	77.1	2203	2	T42742
12	35	72.9	180	2	T47414
13	35	72.9	199	2	AC3241
14	35	72.9	371	2	T26389
15	35	72.9	400	2	T41569
16	35	72.9	457	2	UC5422
17	35	72.9	468	2	S45145
18	35	72.9	471	1	S14733
19	35	72.9	471	2	H84363
20	35	72.9	699	2	A47296
21	35	72.9	1023	2	A47296
22	34.5	71.9	553	2	T06499
23	34	70.8	205	2	D71918
24	34	70.8	290	2	S36706
25	34	70.8	304	2	T42554
26	34	70.8	312	2	T50960
27	34	70.8	326	2	T29810
28	34	70.8	326	2	US0169
29	34	70.8	392	2	AB2474

30	34	70.8	411	2	A96985	uncharacterized co
31	34	70.8	423	2	B64157	hypothetical prote
32	34	70.8	432	2	B65190	potassium uptake p
33	34	70.8	432	2	A91226	potassium uptake p
34	34	70.8	433	2	G86072	trk system potassi
35	34	70.8	483	2	AB0458	methionine-CRNA 11
36	34	70.8	547	2	D84942	methionine-CRNA 11
37	34	70.8	550	2	H81718	methionine-CRNA 11
38	34	70.8	550	2	C71567	methionine-CRNA 11
39	34	70.8	551	2	H72117	methionine-CRNA 11
40	34	70.8	551	2	C86506	methionine-CRNA 11
41	34	70.8	551	2	H81552	methionine-CRNA 11
42	34	70.8	658	2	D69431	methionine-CRNA 11
43	34	70.8	675	2	AF0185	methionine-CRNA 11
44	34	70.8	677	1	SYECMT	methionine-CRNA 11
45	34	70.8	677	2	AH0776	methionine-CRNA 11
46	34	70.8	677	2	C83210	methionine-CRNA 11
47	34	70.8	677	2	C85839	methionine-CRNA 11
48	34	70.8	677	2	H90993	methionine-CRNA 11
49	34	70.8	682	2	164113	methionine-CRNA 11
50	34	70.8	702	2	C82792	methionyl-CRNA syn
51	34	70.8	731	2	D82249	methionyl-CRNA syn
52	34	70.8	734	2	B70173	methionine-CRNA 11
53	34	70.8	797	2	T05247	methionine-CRNA 11
54	34	70.8	917	2	T22898	hypothetical prote
55	34	70.8	989	2	T02568	hypothetical prote
56	34	70.8	1131	2	A23944	chitin synthase (E
57	34	68.8	164	2	E81942	probable 2-amino-4
58	34	68.8	164	2	H81162	2-amino-4-hydroxy-
59	33	68.8	210	2	AC0667	ribulose-phosphate
60	33	68.8	246	2	G88366	protein C04H5.4 [1
61	33	68.8	483	2	G81745	conserved hypochet
62	33	68.8	483	2	AE0914	trk system potassi
63	33	68.8	503	2	T18933	hypothetical prote
64	33	68.8	503	2	G96552	unknown protein, 6
65	33	68.8	512	2	F83761	fumate hydratase
66	33	68.8	512	2	T37180	probable membrane
67	33	68.8	530	2	T18932	hypothetical prote
68	33	68.8	554	2	G82272	DNA repair protein
69	33	68.8	554	2	A81246	methionyl-CRNA syn
70	33	68.8	685	2	G82022	methionine-CRNA 11
71	33	68.8	811	2	E71281	methionine-CRNA 11
72	33	68.8	1955	2	T41170	probable 1,3-beta-
73	32	66.7	50	2	H97855	hypothetical prote
74	32	66.7	139	2	E70925	hypothetical prote
75	32	66.7	319	2	S35928	6-phosphofructokin
76	32	66.7	322	2	T40718	probable transmemb
77	32	66.7	324	2	A37767	stress-inducible p
78	32	66.7	384	2	H84405	hypothetical prote
79	32	66.7	418	2	T34606	probable fumarylac
80	32	66.7	463	2	AP0469	probable permease
81	32	66.7	472	2	G01872	seleulin-binding p
82	32	66.7	572	2	S72249	trithorax protein
83	32	66.7	581	2	S62505	probable alpha-amy
84	32	66.7	588	2	A26158	decapentaplegic pr
85	32	66.7	598	2	T51368	gamma-aminobutyric
86	32	66.7	598	2	T52207	hypothetical prote
87	32	66.7	599	2	D83764	chitinase Bh0916 [
88	32	66.7	612	2	E97790	antipeptidase hom
89	32	66.7	795	2	AD0296	phenylalanine-CRNA
90	32	66.7	1174	1	HJBYDH	helicase (EC 3.6.1
91	32	66.7	1231	2	AF2220	hypothetical prote
92	32	66.7	1337	2	T00209	MEGF8 protein - hu
93	32	65.6	357	2	B47411	ADP-ribosylarginine
94	31.5	65.6	362	2	A47411	ADP-ribosylarginine
95	31.5	65.6	362	2	A38135	ADP-ribosylarginine
96	31	64.6	99	2	G95971	hypothetical expor
97	31	64.6	145	2	AD2855	hypothetical prote
98	31	64.6	192	2	AH3643	cytochrome b561 [i
99	31	64.6	199	2	AB3172	conserved hypochet
100	31	64.6	205	2	T43554	ubiquitin fusion d

## ALIGNMENTS

## RESULT 1

KIRRC

protein kinase C (EC 2.7.1.1) epsilon - rabbit

C/Species: *Oryctolagus cuniculus* (domestic rabbit)

C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 05-Oct-2004

C/Accession: A29880

R/Org: S.; Akita, Y.; Konno, Y.; Imajoh, S.; Suzuki, K.

Cell 53, 731-741, 1988

A/Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to the P

A/Reference number: A29880; MUID:88223367; PMID:3370672

A/Accession: A29880

A/Molecule type: mRNA

A/Residues: 1-736 &lt;OHN&gt;

A/Cross-references: UNIPARC:UPI0000172502; GB:M20014

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A/Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl

C/Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bl

C/Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b

F/156-161/Region: pseudophosphorylation motif

F/170-220/Domain: protein kinase C zinc-binding repeat homology &lt;K21&gt;

F/243-292/Domain: protein kinase C zinc-binding repeat homology &lt;K22&gt;

F/406-667/Domain: protein kinase homology &lt;KIN&gt;

F/414-422/Region: protein kinase ATP-binding motif

F/1170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F/183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F/243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F/256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F/437,455,531,533/Active site: Lys, Glu, Asp, Lys #status predicted

F/703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 48; DB 1; Length 736;

Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8

Db 85 HDAPIGVD 92

## RESULT 2

KIMSCB

protein kinase C (EC 2.7.1.1) epsilon - mouse

C/Species: *Mus musculus* (house mouse)

C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 05-Oct-2004

C/Accession: S02270

R/Schnap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.

FBS Lett. 243, 351-357, 1989

A/Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a ratio

A/Reference number: S02270; MUID:89137541; PMID:2917656

A/Accession: S02270

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-737 &lt;SCH&gt;

A/Cross-references: UNIPROT:P16054; UNIPARC:UPI0000029722

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A/Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl

C/Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bl

C/Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b

F/156-161/Region: pseudophosphorylation motif

F/170-220/Domain: protein kinase C zinc-binding repeat homology &lt;K21&gt;

F/243-292/Domain: protein kinase C zinc-binding repeat homology &lt;K22&gt;

F/406-667/Domain: protein kinase homology &lt;KIN&gt;

F/414-422/Region: protein kinase ATP-binding motif

F/170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F/183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F/243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F/256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F/437,455,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

F/703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi

Query Match 100.0%; Score 48; DB 1; Length 737;

Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8

Db 85 HDAPIGVD 92

## RESULT 3

KIRRC

protein kinase C (EC 2.7.1.1) epsilon - rat

C/Species: *Rattus norvegicus* (Norway rat)

C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 05-Oct-2004

C/Accession: B28163; B26408; S00216

R/Org: Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igaseh, K.; Nishizuka, Y.

U. Biol. Chem. 263, 6927-6932, 1988

A/Title: The structure, expression, and properties of additional members of the protein y

A/Reference number: A92717; MUID:88198270; PMID:2834397

A/Accession: B28163

A/Molecule type: DNA

A/Residues: 1-737 &lt;ONQ&gt;

A/Cross-references: UNIPROT:P09216; UNIPARC:UPI000012056D; GB:M18331; NID:9206182; PIDN:1

R/Housey, G.M.; O'Brien, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.

Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987

A/Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kina

A/Reference number: A94145; MUID:87147193; PMID:3469647

A/Accession: B26408

A/Molecule type: mRNA

A/Residues: 397-447; GQGRGLHDDREDFSGAGET, 467, USNPTLLIPQGPPLLRQ, 487-545, C, 547-636

A/Cross-references: UNIPARC:UPI000006662B; GB:M15523; NID:9206192; PIDN:AAA41877.1; PIDN

C/Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene ar

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A/Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl

C/Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bl

C/Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester b

F/156-161/Region: pseudophosphorylation motif

F/170-220/Domain: protein kinase C zinc-binding repeat homology &lt;K21&gt;

F/243-292/Domain: protein kinase C zinc-binding repeat homology &lt;K22&gt;

F/406-667/Domain: protein kinase homology &lt;KIN&gt;

F/414-422/Region: protein kinase ATP-binding motif

F/170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F/183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F/243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F/256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F/437,455,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

F/703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 48; DB 1; Length 737;

Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8

Db 85 HDAPIGVD 92

## RESULT 4

S28942

protein kinase C (EC 2.7.1.1) epsilon - human

C/Species: *Homo sapiens* (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Oct-2004

C/Accession: S28942

R/Baeta, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.

Biochim. Biophys. Acta 1132, 154-160, 1992

A/Title: Sequence and expression of human protein kinase C-epsilon.

A/Reference number: S28942; MUID:93003318; PMID:1382605

A/Accession: S28942

A/Status: preliminary



A/Molecule type: mRNA  
A/Residues: 1-737 <BAS>  
A/Cross-references: UNIPROT:O02156; UNIPARC:UPI000012DF6B; EMBL:X65293; NID:g35494; PIDN  
C/Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-  
of inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester  
C/Genetics:  
A/Gene: GDB:PRKCE  
A/Cross-references: GDB:128039; OMIM:176975  
A/Map position: 3pter-3qter  
C/Function:  
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A/Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl  
C/Superfamily: protein kinase C, delta/epsilon/eta/cheta types; protein kinase C zinc-bi  
C/Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf  
F:156-161/Region: pseudophosphorylation motif  
F:170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>  
F:243-252/Domain: protein kinase C zinc-binding repeat homology <KZ2>  
F:406-668/Domain: protein kinase homology <KIN>  
F:414-422/Region: protein kinase ATP-binding motif  
F:170,201,204,220/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted  
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted  
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted  
F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 100.0%; Score 48; DB 1; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 5  
T39409  
hypothetical protein SPBC13G1.08c - fission yeast (Schizosaccharomyces pombe)  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T39409  
R/Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.  
submitted to the EMBL Data Library, April 1998  
A/Reference number: Z21852  
A/Accession: T39409  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-652 <LYN>  
A/Cross-references: UNIPROT:O60070; UNIPARC:UPI000006ADAC; EMBL:AL022600; PIDN:CAA18661.  
C/Genetics:  
A/Experimental source: strain 972h-; cosmid c13G1  
A/Gene: SPDB:SPBC13G1.08c  
A/Map position: 2

Query Match 81.2%; Score 39; DB 2; Length 652;  
Best Local Similarity 85.7%; Pred. No. 7.9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8  
Db 419 DAPIGYD 425

RESULT 6  
JC4858  
VLDL receptor precursor - African clawed frog  
N/Alternate names: very low density lipoprotein receptor; vitellogenin receptor  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: JC4858  
R/Okabayashi, K.; Shoji, H.; Nakamura, T.; Hashimoto, O.; Asaehina, M.; Sugino, H.  
Biochem. Biophys. Res. Commun. 224, 406-413, 1996  
A/Title: cDNA cloning and expression of the Xenopus laevis vitellogenin receptor.  
A/Reference number: JC4858; MUID:96295501; PMID:8702402

A/Accession: JC4858  
A/Molecule type: mRNA  
A/Residues: 1-869 <OKA>  
A/Cross-references: UNIPROT:O42126; UNIPARC:UPI00000FBB42; GB:AB00606; NID:g2366772; PIDN  
C/Comment: This receptor mediates incorporation of vitellogenin into oocytes.  
C/Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology; I  
C/Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane p  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-869/Product: VLDL receptor #status predicted <MAT>  
F:27-793/Domain: extracellular #status predicted <EXT>  
F:32-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:71-107/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:112-148/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F:153-187/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F:192-228/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F:238-272/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F:277-311/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F:317-354/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F:359-393/Domain: EGF homology <EG1>  
F:399-433/Domain: EGF homology <EG2>  
F:440-479/Domain: LDL receptor WYTD-containing repeat homology <YW1>  
F:480-525/Domain: LDL receptor WYTD-containing repeat homology <YW2>  
F:526-568/Domain: LDL receptor WYTD-containing repeat homology <YW3>  
F:569-612/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F:613-655/Domain: LDL receptor WYTD-containing repeat homology <YW5>  
F:656-698/Domain: LDL receptor WYTD-containing repeat homology <YW6>  
F:707-749/Domain: EGF homology <EG3>  
F:794-815/Domain: transmembrane #status predicted <TM>  
F:816-869/Domain: intracellular #status predicted <CY>  
F:830-834/Region: coated-pit mediated internalization signal  
F:150,201,777,786/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:359-370,366-379,381-393,399-409,405-418,420-433,707-720,716-725,737-749/Dissulfide bond

Query Match 81.2%; Score 39; DB 1; Length 869;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 371 HDAPIGYD 378

RESULT 7  
A39666  
protein kinase C (EC 2.7.1.-) eta - human  
N/Alternate names: protein kinase C PKC-L  
C/Species: Homo sapiens (man)  
C/Date: 08-Nov-1991 #sequence\_revision 11-Apr-1997 #text\_change 05-Oct-2004  
C/Accession: A39666; A42131; S65018  
R/Bacher, N.; Zisman, Y.; Berent, E.; Lävne, E.  
Mol. Cell. Biol. 11, 126-133, 1991  
A/Title: Isolation and characterization of PKC-L, a new member of the protein kinase C-re  
A/Reference number: A39666; MUID:91094824; PMID:1986216  
A/Accession: A39666  
A/Molecule type: mRNA  
A/Residues: 1-276, 'YNENAY', 'SMSSESG', 297-296, 'MRWV', 301, 'PRP', 'GRD', 309-682, 'BA2>  
A/Cross-references: UNIPROT:P24723; UNIPARC:UPI0000172503; GB:M55284; NID:g189988; PIDN:  
R/Bacher, N.; Zisman, Y.; Berent, E.; Lävne, E.  
Mol. Cell. Biol. 12, 1404, 1992  
A/Title: Isolation and characterization of PKC-L, a new member of the protein kinase C-re  
A/Reference number: A42131; MUID:9216874; PMID:1545821  
A/Contents: extratum  
A/Accession: A42131  
A/Molecule type: mRNA  
A/Residues: 277-308 <BA3>  
A/Cross-references: UNIPARC:UPI0000172504; GB:M55284  
A/Note: this report is a revision to reference A39666  
R/Palmer, R.H.; Ridden, J.; Parker, P.J.  
FEBS Lett. 356, 5-8, 1994  
A/Title: Identification of multiple, novel, protein kinase C-related gene products.  
A/Reference number: S51020; MUID:95080426; PMID:7988719  
A/Accession: S65018

```
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 437-470, 'E', 472-538 <PAL>
A:Cross-references: UNIPARC:UPI000016B45B; EMBL:S74620; NID:G786485; PIDN:AA832724.1; P2
C:Genetics:
A:Gene: GDB:PRKCH; PKC-L; PRKCL
A:Cross-references: GDB:129009
A:Map position: 19q13.4-19q13.4
C:Function:
A:Description: catalyzes protein phosphorylation at Ser or Thr residues
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bi
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b
F:117-162/Region: pseudophosphorylation motif
F:117-221/Domain: protein kinase C zinc-binding repeat homology <K21>
F:1246-294/Domain: protein kinase C zinc-binding repeat homology <K22>
F:353-613/Domain: protein kinase homology <KIN>
F:360-369/Region: protein kinase ATP-binding motif
F:117,202,205,221/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:184,187,210,213/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:246,275,278,294/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:259,261,283,286/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:384,403,478,480/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match
Best Local Similarity 79.2%; Score 38; DB 1; Length 682;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 HDAPIGYD 8
Db 88 HETPLGYD 95

RESULT 8
A23690
C:Species: Mus musculus (house mouse)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 05-Oct-2004
C:Accession: A23690
R:Osada, S.; Mizuno, K.; Saigo, T.C.; Akita, Y.; Suzuki, K.; Kuroki, T.; Ohno, S.
J. Biol. Chem. 265, 22434-22440, 1990
A:Title: A phorbol ester receptor/protein kinase, nRKC-eta, a new member of the protein
A:Reference number: A23690; MUID:91093089; PMID:2265135
A:Accession: A23690
A:Molecule type: mRNA
A:Residues: 1-683 <OSA>
A:Cross-references: UNIPROT:P23298; UNIPARC:UPI0000029755; GB:D90242; GB:J05703; NID:922
C:Function:
A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-threonin
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bi
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b
F:158-163/Region: pseudophosphorylation motif
F:117-222/Domain: protein kinase C zinc-binding repeat homology <K21>
F:1246-295/Domain: protein kinase C zinc-binding repeat homology <K22>
F:353-614/Domain: protein kinase homology <KIN>
F:361-369/Region: protein kinase ATP-binding motif
F:117,203,206,222/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:185,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:259,262,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match
Best Local Similarity 79.2%; Score 38; DB 1; Length 683;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 HDAPIGYD 8
Db 88 HETPLGYD 95

RESULT 9
```

```
529478
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C:Accession: I60246; S29478
R:Decker, L.V.; Parker, P.J.; McIntyre, P.
FEBS Lett. 312, 195-199, 1992
A:Title: Biochemical properties of rat protein kinase C-eta expressed in COS cells.
A:Reference number: I60246; MUID:93050193; PMID:11426252
A:Accession: I60246
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-683 <RBS>
A:Cross-references: UNIPROT:Q64617; UNIPARC:UPI000012PF72; EMBL:X68400; NID:956915; PIDN:
C:Function:
A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-threonine
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bi
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid bi
F:117-222/Domain: protein kinase C zinc-binding repeat homology <K21>
F:1246-295/Domain: protein kinase C zinc-binding repeat homology <K22>
F:353-614/Domain: protein kinase homology <KIN>
F:361-369/Region: protein kinase ATP-binding motif
F:117,203,206,222/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:185,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:259,262,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match
Best Local Similarity 79.2%; Score 38; DB 1; Length 683;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 HDAPIGYD 8
Db 88 HETPLGYD 95

RESULT 10
T10259
RNA-directed DNA polymerase (EC 2.7.7.49) - pteromalid wasp (Nasonia vitripennis) retroc
C:Species: Nasonia vitripennis
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10259; I44490
R:Bucke, W.D.; Malik, H.S.; Latche III, W.C.; Blackbush, T.H.
Nature 392, 141-142, 1998
A:Title: Are retrotransposons long-term hitchhikers?
A:Reference number: T10259; MUID:96175715; PMID:9515960
A:Accession: T10259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1025 <NR>
A:Cross-references: UNIPROT:Q03278; UNIPARC:UPI0000131D75; EMBL:L00950; NID:93559783; PI
R:Bucke, W.D.; Blackbush, D.G.; Xiong, Y.; Jakubczak, J.; Blackbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A:Title: Sequence relationship of retrotransposable elements R1 and R2 within and between
A:Reference number: A44490; MUID:93196484; PMID:8383793
A:Accession: I44490
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 314-956, 'Q', 'A', '971', 'AA' <BU2>
A:Cross-references: UNIPARC:UPI000017BF02
A>Note: sequence extracted from NCBI backbone (NCBI:P127243)
C:Genetics:
C:Keywords: nucleotidyltransferase
```

```
Query Match
Best Local Similarity 79.2%; Score 38; DB 2; Length 1025;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 HDAPIGY 7  
|||  
Db 709 HDPIGY 715

## RESULT 11

T42742  
voltage-dependent calcium channel alpha 1 chain, isoform CACNA4 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
C/Accession: T42742  
R/Ihara, Y.; Yamada, Y.; Fujii, Y.; Gonori, T.; Yano, H.; Yasuda, K.; Inagaki, N.; Seino  
Mol. Endocrinol. 9, 121-130, 1995  
A/Title: Molecular diversity and functional characterization of voltage-dependent calcium  
A/Reference number: 222258; MUID:95280950; PMID:7760845  
A/Accession: T42742  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-2203 <IHA>  
A/Cross-references: UNIPARC:UP10000127274; EMBL:D38101; NID:9736711; PIDN:BAA07282.1; PI  
A/Experimental source: Insulinoma RINm5F complementary DNA library  
C/Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
C/Keywords: calcium channel

Query Match 77.1%; Score 37; DB 2; Length 2203;  
Best Local Similarity 85.7%; Pred. No. 74;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
|||  
Db 1937 DSPIGYD 1943

## RESULT 12

T47414  
hypothetical protein T28A8.70 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C/Accession: T47414  
R/Purnelle, B.; Bouctry, M.; Goffeau, A.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X  
submitted to the Protein Sequence Database, March 2000  
A/Reference number: 224466  
A/Accession: T47414  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-180 <PUR>  
A/Cross-references: UNIPROT:Q9LZG9; UNIPARC:UP10000044221; EMBL:AL162691  
A/Experimental source: cultivar Columbia; BAC clone T28A8  
C/Genetics:  
A/Map position: 3  
A/Intons: 21/2; 32/2; 91/3; 105/3  
A/Note: T28A8.70

Query Match 72.9%; Score 35; DB 2; Length 180;  
Best Local Similarity 75.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
|||  
Db 38 HDPIGYD 45

## RESULT 13

AC3241  
conserved hypothetical protein Atu6109 [imported] - Agrobacterium tumefaciens (strain C5  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AC3241  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Kap, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AC3241

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-199 <KUR>  
A/Cross-references: UNIPROT:Q8U626; UNIPARC:UP1000002799; GB:AE008690; PIDN:AAL46345.1;  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: Atu6109  
A/Genome: plasmid

Query Match 72.9%; Score 35; DB 2; Length 199;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
|||  
Db 127 DGPIGYD 133

## RESULT 14

T26389  
hypothetical protein Y105CSB.m - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T26389  
R/McMurray, A.  
submitted to the EMBL Data Library, September 1999  
A/Reference number: 220208  
A/Accession: T26389  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-371 <WIL>  
A/Cross-references: UNIPROT:Q9NAMS; UNIPARC:UP10000061216; EMBL:AL110479; NID:e1542153; I  
A/Experimental source: clone Y105CSB  
C/Genetics:  
A/Gene: CBSP:Y105CSB.m  
A/Intons: 24/1; 56/1; 101/3; 138/2; 219/3; 290/3; 332/2

Query Match 72.9%; Score 35; DB 2; Length 371;  
Best Local Similarity 85.7%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
|||  
Db 59 DLPIGYD 65

## RESULT 15

T41569  
hypothetical protein SPCC736.12c - fission yeast (Schizosaccharomyces pombe)  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T41569  
R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, May 1998  
A/Reference number: 221991  
A/Accession: T41569  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-400 <MO>  
A/Cross-references: UNIPROT:O74958; UNIPARC:UP10000178200; EMBL:AL023705; PIDN:CAA19276.1  
A/Experimental source: strain 972h-; cosmid c736  
C/Genetics:  
A/Gene: SPDB:SPCC736.12c  
A/Map position: 3  
A/Intons: 29/1; 349/1

Query Match 72.9%; Score 35; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIG 6  
| | | | |  
DB 76 HDAPIG 81

## RESULT 16

FK506-binding protein, FKBP51 - human  
N/Alternate names: peptidyl prolyl cis-trans isomerase  
C/Species: Homo sapiens (man)  
C/Date: 10-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
C/Accession: J05422  
R/Baugman, G.; Wederrecht, G.J.; Chang, F.; Martin, M.M.; Bourgeois, S.  
Biochem. Biophys. Res. Commun. 232, 437-443, 1997  
A/Title: Tissue distribution and abundance of human FKBP51, an FK506-binding protein the  
A/Reference number: J05422; MUID:97242207; PMID:9125197  
A/Accession: J05422  
A/Molecule type: mRNA  
A/Residues: 1-457 <BAU>  
A/Cross-references: UNIPROT:Q13451, UNIPARC:UPI00000D9EB; GB:U71321; NID:G191640; PIDR  
A/Experimental source: thymus  
C/Comment: This protein catalyzes the cis-to-trans isomerization of peptidyl-prolyl bond  
C/Superfamily: human FK506-binding protein FKBP51; BKB-type peptidylprolyl isomerase hc  
F/50-97/Domain: BKB-type peptidylprolyl isomerase homology <PPI>  
F/317-350/Domain: tetratricopeptide repeat homology <TR1>  
F/351-384/Domain: tetratricopeptide repeat homology <TR2>

Query Match 72.9%; Score 35; DB 2; Length 457;  
Best Local Similarity 75.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIG 8  
| | | | |  
DB 196 HDAPIG 203

## RESULT 17

S45145  
H+-transporting two-sector ATPase (EC 3.6.3.14) chain B [validated] - Haloflex volcanii  
N/Alternate names: membrane ATPase  
C/Species: Haloflex volcanii  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 31-Dec-2004  
C/Accession: S55896; S45145; T47204  
R/Steinert, K.; Kroth-Pancic, P.G.; Bickel-Sandkoecker, S.  
Biochim. Biophys. Acta 1249, 137-144, 1995  
A/Title: Nucleotide sequence of the ATPase A- and B-subunits of the halophilic archaeobac  
A/Reference number: S55896; MUID:95322432; PMID:7599166  
A/Accession: S55896  
A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-468 <ST2>  
A/Cross-references: UNIPROT:Q48333; UNIPARC:UPI000013815B; EMBL:X79516; NID:G693938; PID  
A/Experimental source: strain WK340; unicellular; vegetative cells  
C/Genetics:  
A/Gene: atpB  
C/Function:  
A/Description: EC 3.6.3.14 [validated, MUID:97197793]  
C/Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex  
F/183-354/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 72.9%; Score 35; DB 2; Length 468;  
Best Local Similarity 85.7%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIG 8  
| | | | |  
DB 20 DAPIG 26

## RESULT 18

S14733

H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain [validated] - Halobacterium sa  
C/Species: Halobacterium salinarum  
C/Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 31-Dec-2004  
C/Accession: S14733; S18499

R/Rhara, K.; Mukohata, Y.  
Arch. Biochem. Biophys. 286, 111-116, 1991  
A/Title: The ATP synthase of Halobacterium salinarum (halobium) is an archaeobacterial ty  
A/Reference number: S14732; MUID:91378275; PMID:1832829  
A/Accession: S14733  
A/Molecule type: DNA  
A/Residues: 1-471 <IRA>  
A/Cross-references: UNIPROT:P25164; UNIPARC:UPI000013815A; GB:X70294; GB:596356; NID:G434  
A/Note: The source is given as Halobacterium salinarum  
A/Accession: S18499  
A/Molecule type: protein  
A/Residues: 1-8,272-344,425-444,446-469 <IRA2>  
A/Cross-references: UNIPARC:UPI0000172E22; UNIPARC:UPI0000172E23; UNIPARC:UPI0000172E24;  
C/Genetics:  
A/Gene: atpB  
C/Complex: atpA (PIR:S14732) and atpB (PIR:S14733) are the head piece of the ATP synthase  
C/Function:  
A/Description: EC 3.6.3.14 [validated, PMID:9137827]  
A/Note: the alpha chain is considered to be catalytic  
C/Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain }  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding,  
F/1-471/Product: H+-transporting ATP synthase beta chain #status experimental <MAT>  
F/58-65/Region: nucleotide-binding motif A (P-loop)  
F/186-357/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 72.9%; Score 35; DB 1; Length 471;  
Best Local Similarity 85.7%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIG 8  
| | | | |  
DB 20 DAPIG 26

## RESULT 19

H84363  
H+-transporting ATP synthase subunit B [imported] - Halobacterium sp. NRC-1  
C/Species: Halobacterium sp. NRC-1  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004  
C/Accession: H84363  
R/NG, W.V.; Kennedy, S.P.; Malirae, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
A/Title: Genome sequence of Halobacterium species NRC-1.  
A/Reference number: A84160; MUID:20504483; PMID:11016950  
A/Accession: H84363  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-471 <STO>  
A/Cross-references: UNIPROT:Q9HNE4; UNIPARC:UPI0000138159; GB:AB004437; NID:G10581553; P  
C/Genetics:  
A/Gene: atpB

Query Match 72.9%; Score 35; DB 2; Length 471;  
Best Local Similarity 85.7%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIG 8  
| | | | |  
DB 20 DAPIG 26

## RESULT 20

A38368  
chitinase (EC 3.2.1.14) precursor - Bacillus circulans  
C/Species: Bacillus circulans  
C/Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 09-Jul-2004

C;Accession: A38368  
R;Matnabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.  
J. Biol. Chem. 265, 15659-15665, 1990  
A;Title: Gene cloning of chitinase A1 from *Bacillus circulans* WL-12 revealed its evolution  
A;Reference number: A38368; MUID:90368776; PMID:2203782  
A;Accession: A38368  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-699 <NAT>  
A;Cross-references: UNIPROT:P20533; UNIPARC:UPI00001277E5; GB:M57601; GB:J05599; NID:g10  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 72.9%; Score 35; DB 2; Length 699;  
Best Local Similarity 62.5%; Pred. No. 55;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPICVD 8  
Db 291 HNAFLNYD 298

RESULT 21  
A47296  
thiazide-sensitive electroneutral sodium-chloride cotransporter - winter flounder  
C;Species: *Pseudopleuronectes americanus* (winter flounder)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
A;Accession: A47296  
R;Gamba, G.; Saltzberg, S.N.; Lombardi, M.; Miyashita, A.; Lytton, J.; Hediger, M.A.;  
Proc. Natl. Acad. Sci. U.S.A. 90, 2749-2753, 1993  
A;Title: Primary structure and functional expression of a cDNA encoding the thiazide-sensitive  
A;Reference number: A47296; MUID:93219361; PMID:8464884  
A;Accession: A47296  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-1023 <GAM>  
A;Cross-references: UNIPROT:P55019; UNIPARC:UPI000013541E  
A;Experimental source: urinary bladder  
A;Note: sequence extracted from NCHI backbone (NCBI:128719, NCBI:128720)  
C;Superfamily: rat bumetanide-sensitive Na+/K+/Cl-cotransport protein

Query Match 72.9%; Score 35; DB 2; Length 1023;  
Best Local Similarity 85.7%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8  
Db 52 DAPIGYD 58

RESULT 22  
T06499  
Rieske [2Fe-2S] iron-sulfur protein tic55 - garden pea  
N;Alternate names: cell death suppressor protein homolog  
C;Species: *Pisum sativum* (garden pea)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
A;Accession: T06499  
R;Callebe, A.; Grimm, R.; Kaiser, G.; Luebeck, J.; Soll, J.; Heins, L.  
EMBO J. 16, 7342-7350, 1997  
A;Title: The chloroplastic protein import machinery contains a Rieske-type iron-sulfur  
A;Reference number: 215721; MUID:98070311; PMID:9405363  
A;Accession: T06499  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-553 <CAL>  
A;Cross-references: UNIPROT:O49931; UNIPARC:UPI00000A1DAD; EMBL:AJ000520; NID:g2764523;  
A;Experimental source: cultivar Golf  
C;Genetics: tic55  
C;Keywords: 2Fe-2S; chloroplast; metalloprotein; Rieske iron-sulfur protein  
F;134-181/Domain: Rieske [2Fe-2S] homology <RSK>  
F;144,146,163,166/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status p  
Query Match 71.9%; Score 34.5; DB 2; Length 553;

Best Local Similarity 63.6%; Pred. No. 54;  
Matches 7; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 HDAPICVD---YD 8  
Db 114 HDAPLGLKXVD 124

RESULT 23  
D71918  
hypothetical protein jhp0550 - *Helicobacter pylori* (strain 339)  
C;Species: *Helicobacter pylori*  
A;Variety: strain 339  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
A;Accession: D71918  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doty, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: D71918  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-205 <ARN>  
A;Cross-references: UNIPROT:Q9ZLM9; UNIPARC:UPI00000D71F9; GB:AE001487; GB:AE001439; NID  
C;Genetics: jhp0550  
C;Superfamily: *Helicobacter pylori* hypothetical protein jhp0550

Query Match 70.8%; Score 34; DB 2; Length 205;  
Best Local Similarity 62.5%; Pred. No. 23;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPICVD 8  
Db 70 HDASLGFD 77

RESULT 24  
S36706  
B4 protein - equine herpesvirus 4  
C;Species: equine herpesvirus 4  
C;Date: 09-Jun-1994 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
A;Accession: S36706  
R;Rigbio, P.  
submitted to the EMBL Data Library, November 1989  
A;Reference number: S36703  
A;Accession: S36706  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-290 <RIG>  
A;Cross-references: UNIPROT:Q00039; UNIPARC:UPI0000137BBC; EMBL:X17684; NID:g2578026; PIR  
C;Superfamily: varicella-zoster virus gene 9 protein

Query Match 70.8%; Score 34; DB 2; Length 290;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APIGYD 8  
Db 257 APIGYD 262

RESULT 25  
T42554  
tegument protein - equine herpesvirus 4 (strain NS80567)  
C;Species: equine herpesvirus 4  
A;Variety: strain NS80567  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
A;Accession: T42554  
R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.  
J. Gen. Virol. 79, 1197-1203, 1998

A>Title: The DNA sequence of equine herpesvirus-4.  
A/Reference number: 222173; MUID:98264497; PMID:9603335  
A/Accession: T42554  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-304 <TEU>  
A/Cross-references: UNIPROT:O39253; UNIPARC:UPI00000F2B2C; EMBL:AF030027; NID:G2605950;  
A/Experimental source: strain NS80567  
C/Genetics:  
A/Gene: 11  
C/Superfamily: varicella-zoster virus gene 9 protein

Query Match 70.8%; Score 34; DB 2; Length 304;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 APIGYD 8  
Db 271 APIGYD 276

RESULT 26  
T50960  
related to modulation protein ncdb [imported] - Neurospora crassa  
N/Alternate names: protein B24P7.150  
C/Species: Neurospora crassa  
C/Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004  
R/Schulze, U.; Aign, V.; Hohnes, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, July 2000  
A/Accession: T50960  
A/Reference number: 225286  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-312 <SCH>  
A/Cross-references: UNIPROT:O993S0; UNIPARC:UPI000017B4FE; EMBL:AL389890; GSPDB:GN00116;  
A/Experimental source: BAC clone B24P7; strain OK74A  
C/Genetics:  
A/Gene: NCSP:B24P7.150  
A/Map position: 6

Query Match 70.8%; Score 34; DB 2; Length 312;  
Best Local Similarity 85.7%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 HDAPIGY 7  
Db 249 HDAPIGY 255

RESULT 27  
T29810  
hypothetical protein C46A5.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Sep-2003  
C/Accession: T29810  
R/Johnson, D.; Stellyes, L.  
submitted to the EMBL Data Library, June 1996  
A/Description: The sequence of C. elegans coamid C46A5.  
A/Reference number: 220690  
A/Accession: T29810  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-326 <JOH>  
A/Cross-references: UNIPARC:UPI000017A120; EMBL:U61948; PIDD:AA03143.1; GSPDB:GN00022;  
A/Experimental source: strain Bristol NZ; clone C46A5  
C/Genetics:  
A/Gene: CESP:C46A5.3  
A/Map position: 4  
A/Introns: 91/2

Query Match 70.8%; Score 34; DB 2; Length 326;  
Best Local Similarity 71.4%; Pred. No. 38;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 DAPIGYD 8  
Db 109 DQPIGYD 115

RESULT 28  
J50169  
collagen col-14 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 15-Sep-2003  
C/Accession: J50169  
R/Cox, G.N.; Fields, C.; Kramer, J.M.; Rosenzweig, B.; Hirsch, D.  
Gene 76, 331-344, 1989  
A>Title: Sequence comparisons of developmentally regulated collagen genes of Caenorhabditis  
A/Reference number: A91602; MUID:89326131; PMID:2753356  
A/Accession: J50169  
A/Molecule type: DNA  
A/Residues: 1-326 <COX>  
A/Cross-references: UNIPARC:UPI000016B8BD; GB:M25480; NID:G156251; PIDD:AAA27986.1; PID:G  
C/Genetics:  
A/Gene: col-14  
A/Introns: 91/2  
F/137-166/Domain: helical <HX1>  
F/188-314/Domain: helical <HX2>

Query Match 70.8%; Score 34; DB 2; Length 326;  
Best Local Similarity 71.4%; Pred. No. 38;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8  
Db 109 DQPIGYD 115

RESULT 29  
AB2474  
hypothetical protein al15346 [imported] - Nostoc sp. (strain PCC 7120)  
C/Species: Nostoc sp. PCC 7120  
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AB2474  
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Saeamoto, S.; Matsuda, A.; Itiguchi,  
Nakazaki, T.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: AB2474  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-392 <KUR>  
A/Cross-references: UNIPROT:O8YLF2; UNIPARC:UPI00000CE84D; GB:BA000019; PIDD:BA077045.1;  
A/Experimental source: strain PCC 7120  
C/Genetics:  
A/Gene: al15346

Query Match 70.8%; Score 34; DB 2; Length 392;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 DAPIGY 7  
Db 174 DAPIGY 179

RESULT 30  
A96985  
uncharacterized conserved protein, VanM of Enterococcus faecalis related CAC0691 [import  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: A96985  
R/Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

.: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: A96905  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-411 <KIR>  
A:Cross-references: UNIPROT:Q97L71; UNIPARC:UPI00000C9P4F; GB:AE001437; PIDN:AAK78668.1;  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC0691

Query Match 70.8%; Score 34; DB 2; Length 411;  
Best Local Similarity 62.5%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HDAPIGY 8  
Db 319 HYVPGYD 326

RESULT 31  
B64157  
hypothetical protein HI0723 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 18-Sep-1998  
C:Accession: B64157  
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
R:Goeyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.  
D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: B64157  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-423 <TIGR>  
A:Cross-references: UNIPARC:UPI0000178DFP; GB:U32755; GB:L42023; NID:91573722; PID:91573  
A:Note: best homolog was a hypothetical protein from Escherichia coli  
C:Genetics:  
A:Start codon: GTG  
C:Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 423;  
Best Local Similarity 85.7%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7  
Db 226 HDASIGY 232

RESULT 32  
B65190  
potassium uptake protein trkH [validated] - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C>Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: B65190; S30740; PC2366; A56151; JQ0754  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A:Rose, D.J.; Mau, B.; Siao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: B65190  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-432 <BLAT>  
A:Cross-references: UNIPROT:P21166; UNIPARC:UPI00001681F8; GB:AE000460; GB:U00096; NID:9  
A:Experimental source: strain K-12, substrain MG1655  
R:Daifotis, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.  
Science 257, 771-778, 1992

A:Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 c  
A:Reference number: S30660; MUID:92358234; PMID:1379743  
A:Accession: S30740  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-68, 70-432 <DN>  
A:Cross-references: UNIPARC:UPI000016F69E; EMBL:M87049; NID:9836656; PIDN:AAAG7646.1; PII  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992  
R:Nishimura, K.; Nakayashiki, T.; Inokuchi, H.  
DNA Res. 2, 1-8, 1995  
A:Title: Cloning and identification of the hemG gene encoding protoporphyrinogen oxidase  
A:Reference number: JQ2513; MUID:95308321; PMID:7788523  
A:Accession: PC2366  
A:Molecule type: DNA  
A:Residues: 362-432 <NIS>  
A:Cross-references: UNIPARC:UPI0000178E00  
A:Experimental source: strain VSR751  
R:Schlosser, A.; Meldorf, M.; Stumpe, S.; Bakker, E.P.; Epstein, W.  
J. Bacteriol. 177, 1908-1910, 1995  
A:Title: TrkH and its homolog, TrkG, determine the specificity and kinetics of cation tra  
A:Reference number: A56151; MUID:95204366; PMID:7896723  
A:Accession: A56151  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-417, 'TGVDD', 423, 'SAPASVATLNLGPGGVADVADNFTSMNPVAKWILIANMLFGRLEVFTLLVLPPTPE  
R:Nakahigashi, K.; Inokuchi, H.  
Nucleic Acids Res. 18, 6439, 1990  
A:Title: Nucleotide sequence between the fadB gene and the rna operon from Escherichia c  
A:Reference number: JQ0753; MUID:91057145; PMID:2243799  
A:Accession: JQ0754  
A:Molecule type: DNA  
A:Residues: 1-143, 'T', 144-195, 'S', 197-419, 'G' <NA>  
A:Cross-references: UNIPARC:UPI0000178E01; EMBL:X54687  
C:Genetics:  
A:Gene: trkH  
A:Map position: 86 min  
C:Function:  
A:Description: involved in potassium uptake [validated, MUID:95204366]  
C:Superfamily: potassium uptake protein trkG  
C:Keywords: transmembrane protein

Query Match 70.8%; Score 34; DB 2; Length 432;  
Best Local Similarity 85.7%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7  
Db 226 HDASIGY 232

RESULT 33  
A91226  
potassium uptake protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05  
C:Species: Escherichia coli  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: A91226  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: A91226  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-483 <HAV>  
A:Cross-references: UNIPROT:P21166; UNIPARC:UPI00001373D1; GB:BA000007; PIDN:BA38200.1;  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: BC84777  
C:Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 483;

Best Local Similarity 85.7%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HDAPIGY 7  
|||  
Db 226 HDASIGY 232

## RESULT 34

G86072

potassium uptake protein, requires TrkE [imported] - *Escherichia coli* (strain O157:H7, s

C:Species: *Escherichia coli*

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: G86072

R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: AB5480; MUID:21074935; PMID:11206551

A:Accession: G86072

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <STO>

A:Cross-references: UNIPROT:P21166; UNIPARC:UPI00001373D1; GB:AE005174; NID:g12518727; F

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: trkH

C:Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 483;  
Best Local Similarity 85.7%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## RESULT 35

AB0458

Trk system potassium uptake protein TrkH [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*

C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AB0458

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalil, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AB0458

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <KUR>

A:Cross-references: UNIPROT:O8ZAN2; UNIPARC:UPI00000DC896; GB:AL590842; PIDN:CAC93230.1;

C:Genetics:

A:Gene: trkH

C:Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 483;  
Best Local Similarity 85.7%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## RESULT 36

D84942

methionine-tRNA ligase (EC 6.1.1.10) [imported] - *Buchnera* sp. (strain APS)

N:Alternate names: methionyl-tRNA synthetase

C:Species: *Buchnera* sp.

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-Feb-2003

C:Accession: D84942

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. At

A:Reference number: AB4930; MUID:20445173; PMID:10993077

A:Accession: D84942

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-547 <STO>

A:Cross-references: UNIPARC:UPI00005846F; GB:AP000398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: metG; BUI09

C:Superfamily: methionyl-tRNA synthetase

C:Keywords: ligase

Query Match 70.8%; Score 34; DB 2; Length 547;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 37

H81718

methionyl-tRNA synthetase TC0301 [imported] - *Chlamydia muridarum* (strain N195)

C:Species: *Chlamydia muridarum*

C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: H81718

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.

C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.

A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: H81718

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-550 <TEB>

A:Cross-references: UNIPROT:Q9PL07; UNIPARC:UPI00005788D; GB:AE002297; GB:AE002160; NID

A:Experimental source: strain N195 (MoPn)

C:Genetics:

A:Superfamily: methionyl-tRNA synthetase

Query Match 70.8%; Score 34; DB 2; Length 550;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 38

C71567

methionine-tRNA ligase (EC 6.1.1.10) - *Chlamydia trachomatis* (serotype D, strain UM3/Cx)

C:Species: *Chlamydia trachomatis*

C>Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004

C:Accession: C71567

R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia traci*

A:Reference number: A71570; MUID:99000809; PMID:9784135

A:Accession: C71567

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-550 <ARN>

A:Cross-references: UNIPROT:O84035; UNIPARC:UPI0000047BF6; GB:AB001277; GB:AB001273; NID

A:Experimental source: serotype D, strain UM-3/Cx

C:Genetics:



Job time : 40 secs

A:Gene: metC  
 C:Superfamily: methionyl-tRNA synthetase  
 C:Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 70.8%; Score 34; DB 2; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGY 7  
 |||||  
 Db 253 DAPIGY 258

## RESULT 39

H72117  
 methionine-tRNA ligase (EC 6.1.1.10) - Chlamydomonas reinhardtii (strain CWL029)  
 C:Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: H72117  
 R:Kaitman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
 Nature Genet. 21, 385-389, 1999  
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
 A:Reference number: A72000; MUID:99206606; PMID:10192388  
 A:Accession: H72117  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-551 <ARN>  
 A:Cross-references: UNIPROT:Q92959, UNIPARC:UPI0000165616; GB:AE001598; GB:AE001363; NID  
 A:Experimental source: strain CWL029  
 C:Genetics:  
 A:Gene: metC  
 C:Superfamily: methionyl-tRNA synthetase  
 C:Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 70.8%; Score 34; DB 2; Length 551;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGY 7  
 |||||  
 Db 252 DAPIGY 257

## RESULT 40

C86506:  
 methionyl-tRNA synthetase [imported] - Chlamydomonas reinhardtii (strain J138)  
 C:Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: C86506  
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tribuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie  
 Nucleic Acids Res. 28, 2311-2314, 2000  
 A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
 A:Reference number: A86491; MUID:20330349; PMID:10871362  
 A:Accession: C86506  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-551 <STO>  
 A:Cross-references: UNIPROT:Q92959, UNIPARC:UPI000013658B; GB:BA000008; NID:g8978496; PI  
 A:Experimental source: strain J138  
 C:Genetics:  
 A:Gene: metC  
 C:Superfamily: methionyl-tRNA synthetase

Query Match 70.8%; Score 34; DB 2; Length 551;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGY 7  
 |||||  
 Db 252 DAPIGY 257

Search completed: December 3, 2005, 23:29:13

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 23:28:09 / Search time 226 Seconds  
(without alignments)  
24.974 Million cell updates/sec

Title: US-10-807-553-2

Perfect score: 48

Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	125	2	08C944 MOUSE
2	48	100.0	735	1	KPCE_RABIT
3	48	100.0	737	1	KPCE_HUMAN
4	48	100.0	737	1	KPCE_MOUSE
5	48	100.0	737	1	KPCE_RAT
6	48	100.0	737	2	06DUV1 RAT
7	48	100.0	754	2	04SG88 TETNG
8	48	100.0	895	2	04T021 TETNG
9	44	91.7	118	2	04TFB5 TETNG
10	44	91.7	766	2	04RM42 TETNG
11	41	85.4	774	2	08D965 VIBVU
12	41	85.4	800	2	07MLA7 VIBVU
13	40	83.3	887	2	06GNZ7 XENLA
14	39	81.2	421	2	06GN9D6 RHOPA
15	39	81.2	586	2	08H055 ORISA
16	39	81.2	652	2	06O070 SCHPO
17	39	81.2	731	2	08H922 ORYSA
18	39	81.2	861	2	05S0S2 CRYNE
19	39	81.2	861	2	05KFE2 CRYNE
20	39	81.2	869	2	04A126 XENLA
21	39	81.2	869	2	06NS01 XENLA
22	38	79.2	121	2	07IUV9 HUMAN
23	38	79.2	683	1	KPCL_HUMAN
24	38	79.2	683	1	KPCL_MOUSE
25	38	79.2	683	1	KPCL_RAT
26	38	79.2	683	2	08NE03 HUMAN
27	38	79.2	683	2	08K2K8 MOUSE
28	38	79.2	1025	1	POZ1_NASVI
29	37	77.1	493	2	04KB20 PSEFS
30	37	77.1	493	2	04A320 HIPCN
31	37	77.1	685	2	04PGX8 USTMA

32	37	77.1	695	2	091WX8 RAT	091WX8 ratus norv
33	37	77.1	2203	1	CACID1 RAT	P27732 ratus norv
34	36	75.0	213	2	06D7L9 ERWCT	06D779 erwila car
35	36	75.0	229	2	08U140 XENLA	08U140 xenopus lae
36	36	75.0	461	2	04PD5 USTVA	04PD5 ustlago ma
37	35	72.9	66	2	069S31 ORYSA	069S31 oryza sativ
38	35	72.9	171	2	09F5F3 AGRRH	09F5F3 agrobacteri
39	35	72.9	180	2	09LZG9 ARATP	09LZG9 arabidopsis
40	35	72.9	199	2	09R6J9 PRHIZ	09R6J9 agrobacteri
41	35	72.9	199	2	08U626 AGRRS	08U626 agrobacteri
42	35	72.9	218	2	08XHB1 CLOPE	08XHB1 clostridium
43	35	72.9	226	2	04L708 STAPU	04L708 staphylococ
44	35	72.9	229	2	08FBL7 BC046	08FBL7 escherichia
45	35	72.9	233	2	07ZXG7 XENLA	07ZXG7 xenopus lae
46	35	72.9	238	2	04FT28 PGAMW	04FT28 psychrobact
47	35	72.9	257	2	0726G2 DESVH	0726G2 desulfovibr
48	35	72.9	260	2	082KS7 STRWM	082KS7 streptomyce
49	35	72.9	330	2	059EB8 HUMAN	059EB8 homo sapien
50	35	72.9	336	2	05VKR1 SACER	05VKR1 saccharopol
51	35	72.9	351	2	062BK2 CAERL	062BK2 caenorhabdi
52	35	72.9	371	2	09NAM5 CAERL	09NAM5 caenorhabdi
53	35	72.9	385	2	08S0S1 ORYSA	08S0S1 oryza sativ
54	35	72.9	402	2	08KNG9 MICEC	08KNG9 micromosp
55	35	72.9	437	2	074958 SCHPO	074958 schizosacch
56	35	72.9	449	2	0646T7 CHICK	0646T7 gallus gall
57	35	72.9	456	1	KFBP5 MOUSE	064378 mus musculu
58	35	72.9	456	2	06ZR21 HUMAN	06ZR21 homo sapien
59	35	72.9	456	2	05U2T9 RAT	05U2T9 ratus norv
60	35	72.9	456	2	04FJN2 MOUSE	04FJN2 mus musculu
61	35	72.9	457	1	KFBP5 AOTNA	09X11 aotus nancy
62	35	72.9	457	1	KFBP5 CERAE	09S105 ceropichne
63	35	72.9	457	1	KFBP5 HUMAN	013451 h fks06-din
64	35	72.9	457	1	KFBP5 SAGOE	09X812 saginus oe
65	35	72.9	457	1	KFBP5 SA1BB	09X815 saimiri bol
66	35	72.9	457	2	05TGM6 HUMAN	05TGM6 homo sapien
67	35	72.9	457	2	053GX4 HUMAN	053GX4 homo sapien
68	35	72.9	468	1	VATB_HALVO	048333 halobacteri
69	35	72.9	471	1	VATB_HALVO	09H964 halobacteri
70	35	72.9	483	2	067B65 SCHUR	067B65 dehalococco
71	35	72.9	552	2	04H2P4 GIBZE	04H2P4 gibberella
72	35	72.9	581	2	07SAF7 NEURO	07SAF7 neurospora
73	35	72.9	591	2	05EB14 VIBF1	05EB14 vibrio vuln
74	35	72.9	611	2	08DDZ2 VIBVU	08DDZ2 vibrio vuln
75	35	72.9	611	2	07MPR4 VIBVU	07MPR4 vibrio vuln
76	35	72.9	644	2	08CWN1 STAPD	08CWN1 staphylococ
77	35	72.9	644	2	05HMH0 STAPD	05HMH0 staphylococ
78	35	72.9	657	2	063KY9 BURMA	063KY9 burkholderi
79	35	72.9	657	2	062CS0 BURMA	062CS0 burkholderi
80	35	72.9	699	1	CH1A1 BACCI	060533 bacillus ci
81	35	72.9	785	2	0869D6 ASCCS	0869D6 acidithiobac
82	35	72.9	795	2	053N63 ORYSA	053N63 oryza sativ
83	35	72.9	924	1	GLNE_ACIAD	06F619 actinobact
84	35	72.9	943	2	07S3J2 NEUCR	07S3J2 neurospora
85	35	72.9	1023	1	512A3 PSEAM	05S019 pseudopleu
86	35	72.9	1429	2	05G2S4 BRARE	05G2S4 brachydanio
87	35	71.9	553	2	049931 PEBA	049931 pisum sativ
88	34.5	70.8	148	2	063QD5 BURPS	063QD5 burkholderi
89	34	70.8	156	2	084KA1 GASPA	084KA1 crocus sati
90	34	70.8	177	2	09EUW4 LISIN	09EUW4 listeria in
91	34	70.8	180	2	062G44 BURMA	062G44 burkholderi
92	34	70.8	183	2	04L145 BURUR	04L145 burkholderi
93	34	70.8	194	2	06M0G1 METWP	06M0G1 methanococc
94	34	70.8	205	2	09ZLM9 HELPO	09ZLM9 helicobacte
95	34	70.8	216	2	072VP1 LEPTC	072VP1 leptospira
96	34	70.8	226	2	08CXU6 LEPTC	08CXU6 leptospira
97	34	70.8	221	2	041606 GIBZE	041606 gibberella
98	34	70.8	222	2	06C524 YARLI	06C524 yarrowia li
99	34	70.8	223	2	08F4F3 LEPTN	08F4F3 leptospira
100	34	70.8	223	2		

## ALIGNMENTS

RESULT 1  
 Q8C944 MOUSE PRELIMINARY; PRT; 125 AA.  
 AC Q8C944  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length  
 DE enriched library, clone:A730046G04 product:protein kinase C, epsilon,  
 DE full insert sequence.  
 GN Name=PrKc;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX Medline=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RT Carninci P., Hayashizaki Y.;  
 RL "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Izawa A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Maceno Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Stuhli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okubo T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guestinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontuski S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsuki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume M.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirozawa T.,  
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1-SIMILARITY: Contains 1 C2 domain.  
 DR EMBL; AK042994; BAC11430.1; -, mRNA.  
 DR HSPB; P09216; IGM1.  
 DR SMR; Q8C944; 1-116.  
 DR Ensembl; ENSMUSG00000045038; Mus musculus.  
 DR MGJ; MGJ:97599; PrKce.  
 DR GO; GO:0016301; P:kinase activity; IEA.  
 DR InterPro; IPR000008; C2.  
 DR Pfam; PF00168; C2; 1.  
 DR PRINTS; PR00360; C2DOMAIN.  
 DR SMART; SM00239; C2; 1.  
 DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
 KW Kinase.  
 SQ SEQUENCE 125 AA; 14137 MW; 5885D11F6BF5C5C5 CRC64;  
 QY 1 HDAPIGYD 8  
 DB 85 HDAPIGYD 92  
 RESULT 2  
 KCPE RABIT  
 ID KCPE RABIT STANDARD; PRT; 736 AA.  
 AC P10830;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Protein kinase C, epsilon type (BC 2.7.1.1-) (nPKC-epsilon).  
 GN Name=PRKc; cuniculus (Rabbit).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
 OC Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (mRNA).  
 RC MEDLINE=88223367; PubMed=3370672; DOI=10.1016/0092-8674(88)90091-8;  
 RX Ohno S., Akita Y., Konno Y., Imaizumi S., Suzuki K.;  
 RA "A novel phospholipid receptor/protein kinase, nPKC, distantly  
 RT related to the protein kinase C family.";  
 RL Cell 53:731-741(1988).  
 RL Cell 53:731-741(1988).  
 CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,  
 CC serine- and threonine-specific enzyme.  
 CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn  
 CC phosphorylates a range of cellular proteins. PKC also serves as  
 CC the receptor for phospholipid esters, a class of tumor promoters.  
 CC -1- PTM: Phosphorylation on Thr-565 triggers autophosphorylation on  
 CC Ser-728 (by similarity).

```

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
CC subfamily.
CC -1- SIMILARITY: Contains 1 C2 domain.
CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M20014; AAA31426.1; -; mRNA.
DR HSSP; P09216; 1GMI.
DR SMR; P10830; 1-136.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_pe_b4.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00130; C1.1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGEDOMAIN.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00479; ZF_DAG_pe_1; 1.
DR PROSITE; PS50081; ZF_DAG_pe_2; 2.
DR ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
DR Phorbol-ester binding; Phosphorylation; Repeat;
DR Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.
FT DOMAIN 1 99
FT ZN_FING 407 667
FT ZN_FING 169 220
FT NP_BIND 242 292
FT ACT_SITE 413 421
FT BINDING 531 531
FT BINDING 436 436
FT MOD_RES 565 565
FT MOD_RES 702 702
FT MOD_RES 709 709
FT MOD_RES 728 728
FT MOD_RES 736 736
FT SEQUENCE 736 AA; 83516 MW; 261C4FE59B9FEB CRC64;
Query Match 100.0%; Score 48; DB 1; Length 736;
Best Local Similarity 100.0%; Pred. NO. 0.59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 HDAPIGVD 8
Db 85 HDAPIGVD 92

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GN Name=PKCE; Synonyms=PKCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleia; Eucarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=30003318; PubMed=1382605; DOI=10.1016/0167-4781(92)90006-L;
RA Batta P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
RA Burns D.J.
RT "Sequence and expression of human protein kinase C-epsilon."
RL Biochim. Biophys. Acta 1132:154-160(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] OF 1-354 AND 480-737.
RX PubMed=1815621; DOI=10.1038/nature03466;
RA Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H.,
RA Muz P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M.,
RA Becker M.C., Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E.,
RA Kremetzki C., Oddy L., Du H., Sun H., Bradshaw-Cordum H., Ali J.,
RA Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C.,
RA Du F., Courtney L., Kalicki J., Ozersky P., Abbott S., Armstrong J.,
RA Belter E.A., Caruso L., Cedroni M., Colton M., Davidson T., Desai A.,
RA Elliott G., Erb T., Fronick C., Gaige T., Haakenson W., Haglund K.,
RA Holmes A., Harkins R., Kim K., Kruchowski S.S., Strong C.M.,
RA McEwan M.D., Goyea E., Hou S., Levy A., Martinka S., Mead K.,
RA Daughin-Kohlberg S., Kozlowski-Reilly A., Shah N.,
RA Swearingen-Shahid S., Snider J., Strong J.T., Thompson J., Yoakum M.,
RA Leonard S., Pearson C., Trant L., Radionenko M., Waligorski J.E.,
RA Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Latreille P.,
RA Wendt M.C., Yang S.-P., Pohl C., Wallis J.W., Speith J., Bieri T.A.,
RA Berkowicz N., Nelson J.O., Osborne J., Ding L., Meyer R., Sabo A.,
RA Shottland Y., Sinha P., Wohldmann P.B., Cook L., Hickenbotham M.T.,
RA Eldred J., Williams D., Jones T.A., She X., Ciccarelli F.D., Huang X.,
RA Izaurralde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X.,
RA McPherson J.D., Mardis E.R., Clifton S.W., Warren W.C.,
RA Chinwalla A.T., Eddy S.R., Marra M.A., Ovcharenko I., Parey T.S.,
RA Miller W., Eichler E.E., Bork P., Suyama M., Torrents D.,
RA Waterston R.H., Wilson R.K.;
RT "Generation and annotation of the DNA sequences of human chromosomes 2
and 4."
RL Nature 434:724-731(2005).
RN [3]
RP PHOSPHORYLATION SITES THR-566 AND SER-729, AND MUTAGENESIS OF LYS-437;
RX THR-566; THR-710 AND SER-729.
RX MEDLINE=21961415; PubMed=11964154; DOI=10.1042/0264-6021.3630537;
RA Cenni V., Doeppler H., Sonnenburg E.D., Maraldi N., Newton A.C.,
RA Toker A.;
RT "Regulation of novel protein kinase C epsilon by phosphorylation."
RL Biochem. J. 363:537-545(2002).
CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -1- PTM: Phosphorylation on Thr-566 by PDPR1 triggers
CC autophosphorylation on Ser-729.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
CC subfamily.
CC -1- SIMILARITY: Contains 1 C2 domain.
CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X65293; CAA46388.1; -; mRNA.
DR EMBL; U51244; AAD08855.1; -; Genomic DNA.
DR EMBL; AC017078; AAY14773.1; -; Genomic DNA.
DR EMBL; AC017006; AAX93253.1; -; Genomic DNA.

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DR PIR; S28942; S28942.  
 DR HSSP; P09216; IGMI.  
 DR SMR; Q02156; 1-136.  
 DR Ensemble; ENSG0000017132; Homo sapiens.  
 DR HGNC; HGNC:9401; PRKCE.  
 DR H-INVD; HIX0019150; -.  
 DR MIM; 116975; -.  
 DR GO; GO:0005624; C:membrane fraction; TAS.  
 DR GO; GO:0004697; F:protein kinase C activity; TAS.  
 DR GO; GO:0004871; F:signal transducer activity; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; TAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR002219; DAG PR bd.  
 DR InterPro; IPR000961; Kinase C.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR Pfam; PF00130; C1\_1; 2.  
 DR Pfam; PF00168; C2\_1.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00433; Kinase C; 1.  
 DR PRINTS; PR00360; C2DOMAIN.  
 DR PRINTS; PR00008; DAGPDOMAIN.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00109; C1; 2.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS50004; C2 DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00479; ZF\_DAG\_PR\_1; 2.  
 DR PROSITE; PS50081; ZF\_DAG\_PR\_2; 2.  
 DR ATP-binding; Kinase; Metal-binding; Nucleotide-binding;  
 KW Phorbol-ester binding; Phosphorylation; Repeat;  
 KW Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.  
 FT DOMAIN 1 99 C2.  
 FT ZN\_FING 408 668 Protein kinase.  
 FT ZN\_FING 242 220 Phorbol-ester/DAG-type 1.  
 FT NP\_BIND 414 422 Phorbol-ester/DAG-type 2.  
 FT ACT\_SITE 532 532 ATP (By similarity).  
 FT BINDING 437 437 Proton acceptor (By similarity).  
 FT MOD\_RES 566 566 ATP (By similarity).  
 FT MOD\_RES 703 703 Phosphothreonine (by PDK1).  
 FT MOD\_RES 710 710 Phosphothreonine (by autocatalysis) (potential).  
 FT MOD\_RES 729 729 Phosphoserine (by autocatalysis) (potential).  
 FT MOD\_RES 729 729 Phosphoserine (by autocatalysis) (potential).  
 FT MUTAGEN 437 437 K->W: Abolishes activity and S-729 phosphorylation.  
 FT MUTAGEN 566 566 T->A: Abolishes phosphorylation by PDK1, and S-729 phosphorylation.  
 FT MUTAGEN 710 710 T->E: No effect on S-729 phosphorylation.  
 FT MUTAGEN 729 729 S->A: No effect on activity; no effect on S-729 phosphorylation.  
 FT MUTAGEN 729 729 S->A: Enhances T-566 dephosphorylation.  
 FT SEQUENCE 737 AA; 83674 MW; 85032D0A091A1F7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 0.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPICGD 8  
 |||||  
 DB 85 HDAPICGD 92

RESULT 4  
 KPCE\_MOUSE

ID KPCE\_MOUSE STANDARD; PRT; 737 AA.  
 AC P16054;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Protein kinase C, epsilon type (BC 2.7.1.1-) (PKC-epsilon).  
 OS Name=Prke; Synonym=Prke; Pkceae;  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=89137541; PubMed=2917656; DOI=10.1016/0014-5793(89)80160-7;  
 RA Schaap D., Parker P.J., Bristol A., Kitz R., Knopf J.;  
 RT "Unique substrate specificity and regulatory properties of PKC-  
 RT epsilon: a rationale for diversity.";  
 RL FEBS Lett. 243:351-357(1989).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=98127436; PubMed=9467942; DOI=10.1038/sj.onc.1201507;  
 RA Wang Q.J., Ace P., Goodnight J., Blumberg P.M., Mischak H.,  
 RA Mushinski J.F.;  
 RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -  
 RT epsilon chimeras, is responsible for conferring tumorigenicity to  
 RT NIH3T3 cells, whereas both regulatory and catalytic domains of PKC-  
 RT epsilon contribute to in vitro transformation.";  
 RL Oncogene 16:53-60(1998).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Wheeler D.L.;  
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,  
 CC serine- and threonine-specific enzyme.  
 CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn  
 CC phosphorylates a range of cellular proteins. PKC also serves as  
 CC the receptor for phorbol esters, a class of tumor promoters.  
 CC -1- PM: Phosphorylation on Thr-566 triggers autophosphorylation on  
 CC Ser-729 (By similarity).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AF028009; AAB84189.1; -; mRNA.  
 CC EMBL; AF325507; AAG3692.1; -; mRNA.  
 CC PIR; S02270; KIMSC.  
 CC HSSP; P09216; IGMI.  
 CC SMR; P16054; 1-136.  
 CC InFAct; P16054; -.  
 CC Ensemble; ENSMUSG00000055637; Mus musculus.  
 CC MGI; MGI:97599; Prke.  
 CC GO; GO:0005737; C:cytoplasm; IDA.  
 CC GO; GO:0005634; C:nucleus; IDA.  
 CC GO; GO:0004699; F:calcium-independent protein kinase C activity; IDA.  
 CC GO; GO:0007635; P:chemosensory behavior; TAS.  
 CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
 CC GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IMP.  
 CC InterPro; IPR000008; C2.  
 CC InterPro; IPR002219; DAG PR bd.  
 CC InterPro; IPR000961; Kinase C.  
 CC InterPro; IPR000719; Prot kinase.  
 CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 CC InterPro; IPR002290; Ser\_thr\_kinase.

DR Pfam; PF00130; Cl.1; 2.  
 DR Pfam; PF00168; C2; 1.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00433; Kinase; C; 1.  
 DR PRINTS; PR00360; C2DOMAIN.  
 DR PRINTS; PR00008; DAGPDOMAIN.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00109; C1; 2.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS50004; C2 DOMAIN; 1.  
 DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00479; ZF\_DAG\_PE\_1; 2.  
 DR PROSITE; PS50081; ZF\_DAG\_PE\_2; 2.  
 DR ATP-binding; Kinase; Metal-binding; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Phosphorylation; Repeat;  
 KM Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.  
 FT DOMAIN 1 99  
 FT ZN\_FING 408 668 Protein kinase.  
 FT ZN\_FING 169 220 Phorbol-ester/DAG-type 1.  
 FT ZN\_FING 242 292 Phorbol-ester/DAG-type 2.  
 FT NP\_BIND 414 422 ATP (By similarity).  
 FT ACT\_SITE 532 532 Proton acceptor (By similarity).  
 FT BINDING 437 437 ATP (By similarity).  
 FT MOD\_RES 566 566 Phosphochreonine (By similarity).  
 FT MOD\_RES 703 703 Phosphochreonine (by autocatalysis) (Potential).  
 FT MOD\_RES 710 710 Phosphochreonine (by autocatalysis) (Potential).  
 FT MOD\_RES 729 729 Phosphoserine (by autocatalysis) (By similarity).  
 FT SEQUENCE 737 AA; 83561 MM; 7AEBBCC10C99F57 CRC64;  
 SQ  
 Query Match 100.0%; Score 48; DB 1; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 0.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RL PFBS Letc. 226:125-128(1987).  
 CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,  
 CC serine- and threonine-specific enzyme.  
 CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn  
 CC phosphorylates a range of cellular proteins. PKC also serves as  
 CC the receptor for phorbol esters, a class of tumor promoters.  
 CC -1- PFM: Phosphorylation on Thr-566 triggers autophosphorylation on  
 CC Ser-729 (By similarity).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 C2 domain.  
 CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.  
 CC This Swiss Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; M18331; AAA41872.1; -; mRNA.  
 DR PIR; B28163; KIRTCF.  
 DR PDB; 1GMT; X-ray; A=1-136.  
 DR RGD; 61925; PKce.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IDA.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR002219; DAG\_PE\_bd.  
 DR InterPro; IPR000961; PKinase\_C.  
 DR InterPro; IPR00719; Prot\_Kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00130; Cl.1; 2.  
 DR Pfam; PF00168; C2; 1.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00433; Kinase; C; 1.  
 DR PRINTS; PR00360; C2DOMAIN.  
 DR PRINTS; PR00008; DAGPDOMAIN.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00109; C1; 2.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS50004; C2 DOMAIN; 1.  
 DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00479; ZF\_DAG\_PE\_1; 2.  
 DR PROSITE; PS50081; ZF\_DAG\_PE\_2; 2.  
 DR 3D-structure; ATP-binding; Kinase; Metal-binding; Nucleotide-binding;  
 KW Phorbol-ester binding; Phosphorylation; Repeat;  
 KM Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.  
 FT DOMAIN 1 99  
 FT ZN\_FING 408 668 Protein kinase.  
 FT ZN\_FING 169 220 Phorbol-ester/DAG-type 1.  
 FT ZN\_FING 242 292 Phorbol-ester/DAG-type 2.  
 FT NP\_BIND 414 422 ATP (By similarity).  
 FT ACT\_SITE 532 532 Proton acceptor (By similarity).  
 FT BINDING 437 437 ATP (By similarity).  
 FT MOD\_RES 566 566 Phosphochreonine (By similarity).  
 FT MOD\_RES 703 703 Phosphochreonine (by autocatalysis) (Potential).  
 FT MOD\_RES 710 710 Phosphochreonine (by autocatalysis) (Potential).  
 FT MOD\_RES 729 729 Phosphoserine (by autocatalysis) (By similarity).  
 FT STRAND 4 16  
 FT HELIX 22 25  
 FT STRAND 40 46  
 FT TURN 47 48  
 FT STRAND 49 53  
 FT STRAND 64 76  
 FT STRAND 78 85  
 FT STRAND 93 101  
 FT HELIX 102 105

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FT TURN 106 106
FT TURN 108 109
FT STRAND 112 118
FT STRAND 120 120
FT STRAND 124 135
SQ SEQUENCE 737 AA; 83478 MW; 6AD6999EFD2659F CRC64;

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 6
O6DVL1 RAT PRELIMINARY; PRT; 737 AA.
ID O6DVL1
AC O6DVL1
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA STRAIN=Mistral; TISSUE=Liver;
RA Buchfield J.G., Schmitz-Peiffer C., Biden T.J.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RL -1- FUNCTION: PKC is activated by diacylglycerol which in turn
phosphorylates a range of cellular proteins. PKC also serves as
the receptor for phorbol esters, a class of tumor promoters (By
similarity).
CC -1- FUNCTION: This is a calcium-activated, phospholipid-dependent,
serine- and threonine-specific enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- COFACTOR: Binds 3 calcium ions per subunit. The ions are bound to
the C2 domain (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AY642593; AAT65503.1; -; mRNA.
DR SMR; O6DVL1; 1-136.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000008; C2
DR InterPro; IPR002219; DAG_Pe_bd.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR InterPro; IPR002290; Ser_Thr_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00130; C1_1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00433; PKinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50004; C2_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00479; ZF_DAG_Pe_1; 2.
DR PROSITE; PS50081; ZF_DAG_Pe_2; 2.
DR AMP-binding; Calcium_Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 737 AA; 83576 MW; CF77776819A26333 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 7
Q4SG88 TETNG PRELIMINARY; PRT; 754 AA.
ID Q4SG88
AC Q4SG88
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 17 SCAP14597, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=STENG00018762001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Tallon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Niclaud S., Jaffe D., Fisher S., Litalia G., Dossat C., Segurens B.,
RA Daehli C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jabin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulsen J., De Bernardis V.,
RA Criand C., Duprat S., Broctier P., Couranceau J.P., Gouy J.,
RA Patra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landt V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander B.S., Weissbach J., Roest Crolius H.;
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RA Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
RL -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
cycle. It is required in higher cells for entry into S-phase and
mitosis. Component of the kinase complex that phosphorylates the
repetitive C-terminus of RNA polymerase II. Catalytic component of
MPF (By similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
mature oocytes (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL; CA501014597; CAG00344.1; -; Genomic_DNA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_Pe_bd.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR InterPro; IPR002290; Ser_Thr_Pkinase.

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DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00130; C1.1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00008; DAGEPDOMAIN.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00479; ZF_DAG_PE_1; 2.
DR PROSITE; PS50081; ZF_DAG_PE_2; 2.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 754 754
SQ SEQUENCE 754 AA; 85146 MW; F9C32DA77EB84DF7 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 754;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPICVD 8
DB 72 HDAPICVD 79

RESULT 8
Q4T021.TETNG
ID Q4T021.TETNG PRELIMINARY; PRT; 895 AA.
AC Q4T021;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome undetermined SCAF11390, whole genome shotgun sequence.
DE (Fragment).
GN ORENAMES=GSTENG0009554001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Desilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ubin C., Castelli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Catalicio L., Poulain J., De Berardinis V.,
RA Ctraud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Landrad-Toh K., Bitren B., Nisham C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
```

```
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -1- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme (By similarity).
CC -1- COFACTOR: Binds 3 calcium ions per subunit. The ions are bound to
CC the C2 domain (By similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL; CAAB01011390; CAF93761.1; -; Genomic_DNA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE_bd.
DR InterPro; IPR000961; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00130; C1.1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00433; Kinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00479; ZF_DAG_PE_1; 1.
DR PROSITE; PS50081; ZF_DAG_PE_2; 2.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 895 895
SQ SEQUENCE 895 AA; 99736 MW; 09C6846992500B55 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 895;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPICVD 8
DB 84 HDAPICVD 91

RESULT 9
Q4T025.TETNG
ID Q4T025.TETNG PRELIMINARY; PRT; 118 AA.
AC Q4T025;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome undetermined SCAF4616, whole genome shotgun sequence.
DE (Fragment).
GN ORENAMES=GSTENG0001687001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Desilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ubin C., Castelli V., Katinka M., Vacherie B.,
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RA Blomont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,  
RA Ctraud C., Dupriet S., Broctier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Lander V., Schachter V., Queller P., Saurin W., Scarpetelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Croliius H.,  
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope, Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -1- SIMILARITY: Contains 1 C2 domain.  
CC EMBL; CAAE01004616; CAF88387.1; -; Genomic\_DNA.  
DR InterPro; IPR000008; C2.  
DR Pfam; PF00168; C2; 1.  
DR PRINTS; PR00360; C2DOMAIN.  
DR SMART; SM00239; C2; 1.  
DR PROSITE; PS50004; C2\_DOMAIN; 1.  
FT NON TER 118  
SQ SEQUENCE 118 AA; 13444 MM; 950C9A4F2B7E08C CRC64;  
Query Match 91.7%; Score 44; DB 2; Length 118;  
Best Local Similarity 87.5%; Pred. No. 0.58;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 HDAPIGYD 8  
Db 84 HDTPIGYD 91  
RESULT 10  
Q4RM42 TETNG PRELIMINARY; PRT; 766 AA.  
AC Q4RM42;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DB Chromosome 10 SCAF15019, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00032218001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,  
RA Mauceli E., Bounaou L., Fischer C., Ozout-Costaz C., Bernot A.,  
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dosset C., Segurens B.,  
RA Dastiv C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthonard V., Rubin C., Castelli V., Katinka M., Vacherie B.,  
RA Blomont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,  
RA Ctraud C., Dupriet S., Broctier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Lander V., Schachter V., Queller P., Saurin W., Scarpetelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Croliius H.,  
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope, Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell  
CC cycle. It is required in higher cells for entry into S-phase and  
CC mitosis. Component of the kinase complex that phosphorylates the  
CC repetitive C-terminus of RNA polymerase II. Catalytic component of  
CC MPF (By similarity).  
CC -1- FUNCTION: This is a calcium-activated, phospholipid-dependent,  
CC serine- and threonine-specific enzyme (By similarity).  
CC -1- COFACTOR: Binds 3 calcium ions per subunit. The ions are bound to  
CC the C2 domain (By similarity).  
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
CC mature oocytes (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC EMBL; CAAE01015019; CAG10540.1; -; Genomic\_DNA.  
DR InterPro; IPR000008; C2.  
DR InterPro; IPR002219; DAG\_PE\_bd.  
DR InterPro; IPR000961; Pkinase\_C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF001245; Tyr\_pkinase.  
DR Pfam; PF00130; C1\_1; 1.  
DR Pfam; PF00168; C2; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase\_C; 1.  
DR PRINTS; PR00360; C2DOMAIN.  
DR PRINTS; PR00008; DAGPEDOMAIN.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00239; C2; 1.  
DR SMART; SM00133; S TK X; 1.  
DR SMART; SM00220; S TKC; 1.  
DR SMART; SM00219; TYKX; 1.  
DR PROSITE; PS50004; C2\_DOMAIN; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00479; ZF\_DAG\_PE\_1; 1.  
DR PROSITE; PS50081; ZF\_DAG\_PE\_2; 1.  
DR ATP-binding; Kinase; Nucleotide-binding;  
DR Serine/threonine-protein kinase; Transferase.  
FT NON TER 766  
SQ SEQUENCE 766 AA; 85776 MM; 588A7229B2AED5AA CRC64;  
Query Match 91.7%; Score 44; DB 2; Length 766;  
Best Local Similarity 87.5%; Pred. No. 4.3;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 HDAPIGYD 8  
Db 84 HDTPIGYD 91  
RESULT 11  
Q8D965 VIBVU PRELIMINARY; PRT; 774 AA.  
AC Q8D965;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE P pilus assembly protein.  
GN OrderedLocNames=VV12741;  
OS Vibrrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.  
OX NCBI\_TaxID=672;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,

RA Choy H.E.;  
RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE016806; AA011085.1; -; Genomic\_DNA.  
DR InterPro; IPR002086; Aldenhyd\_dehydrog.  
DR InterPro; IPR000194; ATPase\_a/bcentre.  
DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; UNKNOWN\_1.  
DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
KM Complete proteome.  
SQ SEQUENCE 774 AA; 86708 MW; C68AAB58F29F6924 CRC64;

Query Match 85.4%; Score 41; DB 2; Length 774;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPICD 8  
Db 654 HNAFLGYD 661

RESULT 12  
Q7MLA7\_VIBVY PRELIMINARY; PRT; 800 AA.  
ID Q7MLA7\_VIBVY PRELIMINARY; PRT; 800 AA.  
AC Q7MLA7;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE P plus assembly protein, porin PapC.  
GN OrderedLocustNames=VVI1520;  
OS *Vibrio vulnificus* (strain VJ016).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.  
OX NCBI\_TaxID=196600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14656965; DOI=10.1101/gr.1295503;  
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,  
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,  
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.;  
RT "Comparative genome analysis of *Vibrio vulnificus*, a marine  
RT pathogen.";  
RL Genome Res. 13:2577-2587(2003).  
DR EMBL; BA00016021; C: integral to membrane; IEA.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0019867; C: outer membrane; IEA.  
DR GO; GO:0015288; F: porin activity; IEA.  
DR InterPro; IPR002086; Aldenhyd\_dehydrog.  
DR InterPro; IPR000194; ATPase\_a/bcentre.  
DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; UNKNOWN\_1.  
DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
KM Complete proteome; Porin.  
SQ SEQUENCE 800 AA; 90024 MW; 499957F81CC88773 CRC64;

Query Match 85.4%; Score 41; DB 2; Length 800;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPICD 8  
Db 680 HNAFLGYD 687

RESULT 13  
Q6GNZ7\_XENLA PRELIMINARY; PRT; 687 AA.  
ID Q6GNZ7\_XENLA PRELIMINARY; PRT; 687 AA.  
AC Q6GNZ7;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
MG80770 Protein.  
GN Name=MG80770;  
OS *Xenopus laevis* (African clawed frog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=SpLeen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhut N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Tohyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=SpLeen;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strusberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*  
RT initiative.";  
RL dev. Dyn. 225:384-391(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=SpLeen;  
RX EMBL; BC073353; AAH73353.1; -; mRNA.  
DR GO; GO:0005524; F: ATP binding; IEA.  
DR GO; GO:0004674; F: protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F: protein-tyrosine kinase activity; IEA.  
DR GO; GO:0007242; P: intracellular signaling cascade; IEA.  
DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000008; C2.  
DR InterPro; IPR002219; DAG\_Pe-bind.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Pkinase C.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00130; C1.1; 2.  
DR Pfam; PF00168; C2.1.  
DR Pfam; PF00069; Pkinase.1.  
DR Pfam; PF00433; Pkinase.C.1.  
DR PRINTS; PR00360; C2DOMAIN.  
DR PRINTS; PR00008; DAGPEDOMAIN.  
DR PRODOM; PD000001; Prot\_kinase; 1.  
DR SMART; SM00109; C1; 2.  
DR SMART; SM00239; C2; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TYRKC; 1.  
DR PROSITE; PSS0004; C2 DOMAIN 2; 1.  
DR PROSITE; PSS00479; DAG\_Pe BIND DOM 1; 2.  
DR PROSITE; PSS00081; DAG\_Pe BIND DOM 2; 2.  
DR PROSITE; PSS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PSS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
SQ SEQUENCE 687 AA; 78400 MW; 6EF3B8D7E1AB6958 CRC64;

Query Match 83.3%; Score 40; DB 2; Length 687;  
 Best Local Similarity 75.0%; Pred. No. 27;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPGYD 8  
 |||||  
 Db 83 HDPIGYD 90

## RESULT 14

06N9D6 RHOPA PRELIMINARY; PRT; 421 AA.  
 ID 06N9D6 RHOPA PRELIMINARY; PRT; 421 AA.  
 AC 06N9D6;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Putative cytochrome P-450 (EC 1.14.--.).  
 GN Rhodospirillum rubrum  
 OS Rhodospirillum rubrum  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Rhodospirillaceae.  
 OC NCBI\_TaxID=1076;  
 CX [1]

## NUCLEOTIDE SEQUENCE.

RA STRAIN=CGA009 / ATCC BAA-98;  
 RX PubMed=14704707; DOI=10.1038/nbt923;  
 RA Lamer F. W., Chain P., Hauser L., Lamerdin J. E., Malfatti S., Doi L.,  
 RA Land M. L., Pelletier D. A., Beatty J. T., Lang A. S., Tabita F. R.,  
 RA Gibson J. L., Hanson T. E., Bobet C., Torres y Torres J. L., Perez C.,  
 RA Harrison F. H., Gibson J., Harwood C. S.,  
 RT "Complete genome sequence of the metabolically versatile  
 RT photosynthetic bacterium Rhodospirillum rubrum".  
 RL Nat. Biotechnol. 22:55-61(2004).  
 CC -1- STRAIN: Belongs to the cytochrome P450 family.  
 DR EMBL; BX572596; CAE27054.1; -; Genomic DNA.  
 DR GO; GO:0046872; F:metal ion binding; IEA.  
 DR GO; GO:0004497; F:monooxygenase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR002397; BP450.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00359; BP450.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN 1.  
 KM Complete proteome; Heme; Iron; Metal-binding; Monooxygenase;  
 KY Oxidoreductase.  
 SQ SEQUENCE 421 AA; 48554 MW; A10F3A5302DAD22F CRC64;

## Query Match

Best Local Similarity 81.2%; Score 39; DB 2; Length 421;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
 |||||  
 Db 97 DAPIGYD 103

## RESULT 15

08H055 ORYZA PRELIMINARY; PRT; 586 AA.  
 ID 08H055 ORYZA PRELIMINARY; PRT; 586 AA.  
 AC 08H055;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Putative DHHC-type zinc finger protein.  
 GN Name=OSUNBA0014006.17;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Lilliales; Poales; Poaceae;  
 OC Eriocaulaceae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=39947;  
 CX [1]

RP NUCLEOTIDE SEQUENCE.  
 RA Wang R. A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saeki C.,  
 RA Currie J., Collura K.,  
 RL Submitted (JBC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; ACJ05928; AAN77310.1; -; Genomic DNA.

DR Gramene; Q8H055;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0046872; F:metal ion binding; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001594; Znf\_DHHC.  
 DR Pfam; PF01529; zf-DHHC; 1.  
 DR ProDom; PD003041; Znf\_DHHC; 1.  
 DR PROSITE; PS50216; ZF\_DHHC; 1.  
 SQ SEQUENCE 586 AA; 64254 MW; 2AFAF228BA31F3A CRC64;

Query Match 81.2%; Score 39; DB 2; Length 586;  
 Best Local Similarity 75.0%; Pred. No. 36;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPGYD 8  
 |||||  
 Db 408 HDVPIGHD 415

## RESULT 16

060070 SCHPO PRELIMINARY; PRT; 652 AA.  
 ID 060070 SCHPO PRELIMINARY; PRT; 652 AA.  
 AC 060070;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DE SPAC13G1.08c protein (Ash2 protein).  
 GN Name=ash2; ORFNames=SPAC13G1.08c;  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
 OC NCBI\_TaxID=4896;  
 CX [1]

## NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA STRAIN=972;  
 RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;  
 RA Wood V., Gwilliam R., Rajandream M. A., Lyne M. H., Lyne R., Stewart A.,  
 RA Sgouros J. G., Past N., Hayles J., Baker S. G., Basham D., Bowman S.,  
 RA Brooks K. D., Brown D., Brown S., Chillingworth T., Churcher C. M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D. R., Hidalgo J., Hodgson G.,  
 RA Holtroyd S., Hornby T., Howarth S., Huckle E. J., Hunt S., Jagsen K.,  
 RA James K. D., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K. L., Murphy L. D., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M. A., Rabinovitch E.,  
 RA Rutherford K. M., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M. N., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R. G., Tivey A., Walsh S. V., Warren T., Whitehead S.,  
 RA Woodward J. R., Voiclaert G., Aert R., Robben J., Grymptre B.,  
 RA Welljens I., Vansteelandt E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,  
 RA Hilbert H., Borzym K., Langer I., Beck A., Lehnach H., Reinhardt B.,  
 RA Pohl T. M., Beger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Huzar S. M.,  
 RA Lucas M., Rochet M., Gallard J., Tallada V. A., Garçon A., Thode G.,  
 RA Dage R. R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bentele J.,  
 RA Dominguez A., Reynelto J. L., Moreno S., Armstrong J., Forsburg S. L.,  
 RA Cerutti L., Lowe T., McCombie W. R., Paulsen I., Potashkin J.,  
 RA Shpakovski G. V., Ussery D., Barrett B. G., Nurse P.,  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 DR EMBL; AL022600; CAA18661.1; -; Genomic DNA.  
 DR PIR; T39409; T39409.  
 DR GeneDB\_Spombe; SPAC13G1.08c; -;  
 DR GO; GO:0048188; C:COMPASS complex; IDA.

DR GO:0048189; C:lid2 complex; IDA.  
DR InterPro: IPR003877; SPRY receptor.  
DR InterPro: IPR001965; Znf\_PHD.  
DR Pfam: PF00622; SPRY. 1.  
DR SMART: SM00249; PHD. 1.  
DR SMART: SM00449; SPRY. 1.  
DR PROSITE: PS01359; ZF\_PHD\_1; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 652 AA; 74252 MW; 998F783EC8BD0360 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 652;  
Best Local Similarity 85.7%; Pred. No. 41;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGYD 8  
DB 419 DAPIGYD 425

RESULT 17  
08H922 ORYSA PRELIMINARY; PRT; 731 AA.  
AC 08H922;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)  
DE Hypothetical protein OSUNB0071K18.2.  
GN ORFNames=OSUNB0071K18.2;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Eubacteriobacteriia; Oryzaceae; Oryza.  
NCBI\_TaxID=33947;

RA NUCLEOTIDE SEQUENCE.  
RA Buell C.R., Yuan Q., Qiyang S., Liu J., Gansberger K., Jones K.M.,  
RA Overton I.L., Teltzin T., Kim M.M., Bera J.J., Jin S.S.,  
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,  
RA Vanaken S.S., Riedmiller S.B., Uteback T.T., Feldblyum T.V.,  
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Feldblyum J.,  
RA White O., Salzberg S.L., Fraser C.M.;  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Buell R.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA The Rice Chromosome 10 Sequencing Consortium;  
RT "In-depth view of structure, activity, and evolution of rice  
RT chromosome 10";  
RL Science 300:1566-1569 (2003).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;  
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AC027038; AA005523.1; -; Genomic\_DNA.  
DR EMBL; AB017103; AAP54178.1; -; Genomic\_DNA.  
DR Gramene; 08H922; -;  
DR GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO:GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO:GO:0008270; F:zinc ion binding; IEA.  
DR InterPro: IPR002035; VWF\_A.  
DR InterPro: IPR001841; Znf\_xing.  
DR Pfam: PF00092; VWA. 1.  
DR Pfam: PF00097; zf-C3HC4. 1.  
DR PRINTS: PR00453; VWFADOMAIN.  
DR SMART: SM00184; RING. 1.  
DR SMART: SM00327; VWA. 1.  
DR PROSITE: PS50234; VWF\_A. 1.  
DR PROSITE: PS50089; ZF\_RING\_2; 1.  
KW Hypothetical protein.

SQ SEQUENCE 731 AA; 78227 MW; 335F9C377831ADU7 CRC64;  
Query Match 81.2%; Score 39; DB 2; Length 731;  
Best Local Similarity 85.7%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGYD 8  
DB 553 DAPIGYD 559

RESULT 18  
Q55Q52 CRYNE PRELIMINARY; PRT; 861 AA.  
AC Q55Q52;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=CNBP2660;  
OS Cryptococcus neoformans var. neoformans B-3501A.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
NCBI\_TaxID=283643;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B-3501A;  
RA Fung B., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
RA Wicks B.L., Fu J., Davis R.W.;  
RT "Cryptococcus neoformans serotype D sequencing";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.

DR EMBL; AA00100032; EAL19939.1; -; Genomic\_DNA.  
DR InterPro: IPR001810; F-box.  
DR InterPro: IPR001680; WD40.  
DR Pfam: PF00646; F-box; 1.  
DR Pfam: PF00400; WD40; 7.  
DR PRINTS: PR00320; GPROTEINRPT.  
DR ProDom: PD000018; WD40; 2.  
DR SMART: SM00256; FBOX. 1.  
DR SMART: SM00320; WD40; 7.  
DR PROSITE: PS50181; FBOX. 1.  
DR PROSITE: PS00678; WD\_REPEATS\_1; 5.  
DR PROSITE: PS50082; WD\_REPEATS\_2; 7.  
DR PROSITE: PS50294; WD\_REPEATS\_REGION. 1.  
KW Hypothetical protein; Repeat; Ub1 conjugation pathway; WD repeat.  
SQ SEQUENCE 861 AA; 95052 MW; B5610A97A6D105FF CRC64;

Query Match 81.2%; Score 39; DB 2; Length 861;  
Best Local Similarity 75.0%; Pred. No. 55;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPGYD 8  
DB 688 HDAPGYD 695

RESULT 19  
Q5KFE2 CRYNE PRELIMINARY; PRT; 861 AA.  
AC Q5KFE2;  
DT 10-MAY-2005 (TReMBLrel. 30, Created)  
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
DE Sulfur metabolite repression control protein, putative.  
GN ORFNames=CNF02050;  
OS Cryptococcus neoformans var. neoformans JEC21.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
NCBI\_TaxID=214684;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN-JEC21;  
 RA lotus B., Amedeo P., Roncaglia P., Vamathavan J., Uterback T.,  
 RA Van Aken S., Fraser C.;  
 RL Submitted (May-2004) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN-JEC21;  
 RA lotus B., Amedeo P., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
 RA Lotus B.J., Fung E., Roncaglia P., Rowley D., Fraser J.A., Allen J.B.,  
 RA Vamathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.B.,  
 RA Boudet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
 RA D'Souza C.A., Fox D.S., Grindberg V., Fu J., Fukushima M., Haas B.U.,  
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Kizyilima M.I.,  
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Maria M.A., Marra R.E.,  
 RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,  
 RA Schein J.E., Shvartbeyn A., Shin H., Shumway M., Specht C.A.,  
 RA Sun B.B., Tenney A., Uterback T.R., Wickes B.L., Wortman J.R.,  
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,  
 RA Fraser C.M., Hyman R.W.;  
 RT "The genome of the basidiomycetous yeast and human pathogen  
 RT *Cryptococcus neoformans*."  
 RL Science 307:1321-1324(2005).  
 DR EMBL; AE017346; AA04020.1; -; Genomic DNA.  
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.  
 DR InterPro; IPR001810; F-box.  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00646; F-box; 1.  
 DR Pfam; PF00400; WD40; 2.  
 DR PRINTS; PR00320; GPROTEINRPT.  
 DR PRODOM; PD000018; WD40; 2.  
 DR SMART; SM00256; FBOX; 1.  
 DR SMART; SM00320; WD40; 7.  
 DR PROSITE; PS00181; FBOX; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 5.  
 DR PROSITE; PS0082; WD\_REPEATS\_2; 7.  
 DR PROSITE; PS0294; WD\_REPEATS\_REGION; 1.  
 DR Complete proteome; Repeat; UBI conjugation pathway; WD repeat.  
 KW SEQUENCE 861 AA; 95078 MW; 93393636195EDC01 CRC64;  
 SQ  
 Query Match 81.2%; Score 39; DB 2; Length 861;  
 Best Local Similarity 75.0%; Pred. No. 55;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HDAPIGYD 8  
 DB 688 HDAPAGFD 695  
 RESULT 20  
 ID 042126 XENLA PRELIMINARY; PRT; 869 AA.  
 AC 042126  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Vitellinogenin receptor.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxId=8335;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Oocyte.  
 RX MEDLINE=96295501; PubMed=8702402; DOI=10.1006/dbrc.1996.1040.  
 RA Okabayashi K., Shoji H., Nakamura T., Hashimoto O., Aashima M.,  
 RA Sugino H.;  
 RT "cDNA cloning and expression of the Xenopus laevis vitellinogenin  
 RT receptor."  
 RL Biochem. Biophys. Res. Commun. 224:406-413(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Oocyte;  
 RA Okabayashi K.;  
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AB006906; BAA22145.1; -; mRNA.  
 DR PIR; JC4858; JC4858.  
 DR HSSP; P01130; 1A1J.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000152; Aex\_hydroxyl\_1\_S.  
 DR InterPro; IPR000742; EGF\_Ca.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR InterPro; IPR000033; LDL\_receptor\_rep.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF07645; EGF\_CA; 1.  
 DR Pfam; PF00057; LDL\_recept\_a; 8.  
 DR Pfam; PF00058; LDL\_recept\_b; 5.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00192; LDLR; 8.  
 DR SMART; SM00135; LY; 5.  
 DR PROSITE; PS0010; ASX\_HYDROXYL; 2.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS50026; EGF\_3; 2.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
 DR PROSITE; PS01209; LDLR\_1; 8.  
 DR PROSITE; PS50068; LDLR\_2; 8.  
 KW Receptor.  
 KW SEQUENCE 869 AA; 96377 MW; A57A3B34072B517 CRC64;  
 SQ  
 Query Match 81.2%; Score 39; DB 2; Length 869;  
 Best Local Similarity 75.0%; Pred. No. 56;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HDAPIGYD 8  
 DB 371 HDPIGYE 378  
 RESULT 21  
 ID 06NS01 XENLA PRELIMINARY; PRT; 869 AA.  
 AC 06NS01;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE VLDLR protein.  
 DE VLDLR protein.  
 GN Name=VLDLR;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxId=8335;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Umed T.B., Toshitsuki S., Carrinci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=23341133; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC070552; AAH70552.1; -; mRNA.  
 DR HSSP; P01130; IAUJ.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR000152; AaX hydroxyl\_S.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR InterPro; IPR000033; LDL\_receptor\_rep.  
 DR Pfam; PF00008; EGF\_1.  
 DR Pfam; PF07645; EGF\_CA; 1.  
 DR Pfam; PF00057; LDL\_recept\_a; 8.  
 DR Pfam; PF00058; LDL\_recept\_b; 5.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 DR SMART; SM00181; EGF; 6.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00192; LDLA; 8.  
 DR SMART; SM00135; LY; 5.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 2.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS50026; EGF\_3; 2.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
 DR PROSITE; PS01209; LDLRA\_1; 8.  
 DR PROSITE; PS50068; LDLRA\_2; 8.  
 DR PROSITE; PS50068; LDLRA\_2; 8.  
 SQ SEQUENCE 869 AA; 96275 MW; 232B982C275B27BD CRC64;  
 Query Match 81.2%; Score 39; DB 2; Length 869;  
 Best Local Similarity 75.0%; Pred. No. 56;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HDAPICVD 8  
 DB 371 HDLPICVE 378  
 RESULT 22  
 ID 071UV9 HUMAN PRELIMINARY; PRT; 121 AA.  
 AC 071UV9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Protein Kinase C eta (Fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 CC Homo.  
 CC NCBI\_TaxID=9606;  
 CC [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skin;

RX MEDLINE=99428533; PubMed=10497222; DOI=10.1074/jbc.274.40.28566;  
 RA Qian T., Fisher G.J.;  
 RT "Cloning and characterization of the human protein kinase C-eta  
 RT promoter.";  
 RL J. Biol. Chem. 274:28566-28574(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skin;  
 RA Qian T.H., Fisher G.J.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 1 C2 domain.  
 DR EMBL; AF045569; AAD12779.1; -; Genomic DNA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR InterPro; IPR000008; C2.  
 DR Pfam; PF00168; C2; 1.  
 DR PRINTS; PR00360; C2DOMAIN.  
 DR SMART; SM00239; C2; 1.  
 DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
 KW Kinase.  
 FT NON TER.  
 SQ SEQUENCE 121 AA; 121 13501 MW; C913189C4A4BAF53 CRC64;  
 Query Match 79.2%; Score 38; DB 2; Length 121;  
 Best Local Similarity 62.5%; Pred. No. 11;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HDAPICVD 8  
 DB 88 HETPLGYD 95  
 RESULT 23  
 ID KPC\_L HUMAN STANDARD; PRT; 682 AA.  
 AC P4723; Q16246;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Protein kinase C, eta type (EC 2.7.1.1-) (PKC-eta) (PKC-L).  
 GN Name=PRKCH; Synonyms=PKCL;  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 CC Homo.  
 CC NCBI\_TaxID=9606;  
 CC [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=91094824; PubMed=1986216;  
 RA Baehar N., Zisman Y., Berent E., Livneh E.;  
 RT "Isolation and characterization of PKC-L, a new member of the protein  
 RT kinase C-related gene family specifically expressed in lung, skin, and  
 RT heart.";  
 RL Mol. Cell. Biol. 11:126-133(1991).  
 RN [2]  
 RP ERRATUM, AND SEQUENCE REVISION.  
 RX MEDLINE=92186874; PubMed=1545821;  
 RA Baehar N., Zisman Y., Berent E., Livneh E.;  
 RL Mol. Cell. Biol. 12:1404-1404(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE OF 437-538.  
 RX MEDLINE=95080425; PubMed=7988719; DOI=10.1016/0014-5793(94)01202-4;  
 RA Palmer R.H., Ridden U., Parker F.J.;  
 RT "Identification of multiple, novel, protein kinase C-related gene  
 RT products.";  
 RL FEBS Lett. 356:5-8(1994).  
 CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,  
 CC serine- and threonine-specific enzyme.  
 CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn  
 CC phosphorylates a range of cellular proteins. PKC also serves as  
 CC the receptor for photol esters, a class of tumor promoters.  
 CC -1- TISSUE SPECIFICITY: Most abundant in lung, less in heart and skin.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC

```

CC      subfamily.
CC      -1- SIMILARITY: Contains 1 C2 domain.
CC      -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; M55284; AAA60100.1; -; mRNA.
CC      EMBL; S74620; AAB32724.1; -; mRNA.
CC      PIR; A39666; A39666.
CC      HSSP; P09216; 1GMI.
CC      Ensemble; ENSG00000027075; Homo sapiens.
CC      HGNC; HGNC:9403; PRKCH.
CC      MIM; 605437; -.
CC      GO; GO:0004697; F:protein kinase C activity; TAS.
CC      GO; GO:0006468; F:protein amino acid phosphorylation; TAS.
CC      GO; GO:0007165; P:signal transduction; TAS.
CC      InterPro; IPR000008; C2.
CC      InterPro; IPR002219; DAG_Pe_bd.
CC      InterPro; IPR000961; Pkinase_C.
CC      InterPro; IPR000719; Prot_kinase.
CC      InterPro; IPR008271; Ser_thr_pkin_AS.
CC      InterPro; IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00168; C2_1; 2.
CC      Pfam; PF00069; Pkinase; 1.
CC      Pfam; PF00433; Pkinase_C; 1.
CC      PRINTS; PR00360; C2DOMAIN.
CC      PRINTS; PR00008; DAGPEDOMAIN.
CC      ProDom; PD000001; Prot_kinase; 1.
CC      SMART; SM00109; C1; 2.
CC      SMART; SM00239; C2; 1.
CC      SMART; SM00133; S_TK_X; 1.
CC      SMART; SM00220; S_TK; 1.
CC      PROSITE; PS50004; C2 DOMAIN; 1.
CC      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC      PROSITE; PS50011; PROTEIN KINASE DOM; 1.
CC      PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC      PROSITE; PS00479; ZF_DAG_Pe_1; 2.
CC      PROSITE; PS50081; ZF_DAG_Pe_2; 2.
CC      ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
CC      Phorbol-ester binding; Repeat; Serine/threonine-protein kinase;
CC      Transferrase; Zinc; zinc-finger.
CC      DOMAIN 12 112 C2..
CC      FT 354 613 Protein kinase.
CC      FT 170 221 Phorbol-ester/DAG-type 1.
CC      FT 244 294 Phorbol-ester/DAG-type 2.
CC      FT 360 368 ATP (By similarity).
CC      FT 478 478 Proton acceptor (By similarity).
CC      FT BINDING 383 383 ATP (By similarity).
CC      FT CONFLICT 471 471 D -> B (in Ref. 3).
CC      SQ SEQUENCE 682 AA; 77563 MW; 13D4EAB013B5AB8 CRC64;

Query Match      79.2%; Score 38; DB 1; Length 682;
Beet Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HDAPIGYD 8
Db      88 HETPIGYD 95

RESULT 24
KACL_MOUSE      STANDARD;      PRT;      683 AA.
AC      P23358;
DT      01-NOV-1991 (Rel. 20, Created)
FT      13-BEP-2005 (Rel. 48, Last annotation update)
DT      Protein kinase C, eta type (EC 2.7.1.1-) (nPKC-eta) (PKC-L).

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GN      Name=Prkch; Synonyms=Pchh;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [mRNA].
RC      TISSUE=Epidermis;
RX      MEDLINE=9103089; PubMed=2266135;
RA      Osada S.I., Mizuno K., Saido T.C., Akita Y., Suzuki K., Kuroki T.,
RA      Ohno S.;
RT      "A phorbol ester receptor/protein kinase, nPKC eta, a new member of
RT      the protein kinase C family predominantly expressed in lung and
RT      skin."
RL      J. Biol. Chem. 265:22434-22440(1990).
CC      -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
CC      serine- and threonine-specific enzyme.
CC      -1- FUNCTION: PKC is activated by diacylglycerol which in turn
CC      phosphorylates a range of cellular proteins. PKC also serves as
CC      the receptor for phorbol esters, a class of tumor promoters.
CC      -1- TISSUE SPECIFICITY: Predominantly expressed in lung and skin.
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
CC      subfamily.
CC      -1- SIMILARITY: Contains 1 C2 domain.
CC      -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; D90242; BAA14288.1; -; mRNA.
CC      PIR; A23690; A23690.
CC      HSSP; P28867; 1PTQ.
CC      Ensemble; ENSMUSG00000021108; Mus musculus.
CC      MGI; MGI:97600; Prkch.
CC      InterPro; IPR000008; C2.
CC      InterPro; IPR002219; DAG_Pe_bd.
CC      InterPro; IPR000961; Pkinase_C.
CC      InterPro; IPR000719; Prot_kinase.
CC      InterPro; IPR008271; Ser_thr_pkin_AS.
CC      InterPro; IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00130; C1_1; 2.
CC      Pfam; PF00168; C2; 1.
CC      Pfam; PF00069; Pkinase; 1.
CC      Pfam; PF00433; Pkinase_C; 1.
CC      PRINTS; PR00360; C2DOMAIN.
CC      PRINTS; PR00008; DAGPEDOMAIN.
CC      ProDom; PD000001; Prot_kinase; 1.
CC      SMART; SM00109; C1; 2.
CC      SMART; SM00239; C2; 1.
CC      SMART; SM00133; S_TK_X; 1.
CC      SMART; SM00220; S_TK; 1.
CC      PROSITE; PS50004; C2 DOMAIN; 1.
CC      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC      PROSITE; PS50011; PROTEIN KINASE DOM; 1.
CC      PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC      PROSITE; PS00479; ZF_DAG_Pe_1; 2.
CC      PROSITE; PS50081; ZF_DAG_Pe_2; 2.
CC      ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
CC      Phorbol-ester binding; Repeat; Serine/threonine-protein kinase;
CC      Transferrase; Zinc; zinc-finger.
CC      DOMAIN 12 102 C2.
CC      FT 355 614 Protein kinase.
CC      FT 171 222 Phorbol-ester/DAG-type 1.
CC      FT 245 295 Phorbol-ester/DAG-type 2.
CC      FT 361 369 ATP (By similarity).
CC      FT 479 479 Proton acceptor (By similarity).
CC      FT BINDING 384 384 ATP (By similarity).
CC      SQ SEQUENCE 683 AA; 77974 MW; C7DB338A9F595576 CRC64;

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Query Match          79.2%; Score 38; DB 1; Length 683;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HDAPICVD 8
Db      88 HETPLGYD 95

RESULT 25
KPCPL RAT          STANDARD; PRT; 683 AA.
ID      064617;
AC      064617;
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Protein Kinase C, eta type (EC 2.7.1.-) (PKC-eta) (PKC-L).
GN      Name=Prkch; Synonym=PKch;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RC      STRAIN=Sprague-Dawley; TISSUE=Lung;
RX      MEDLINE=93050193; PubMed=1426252; DOI=10.1016/0014-5793(92)80934-9;
RA      Dekker L.V., Parker P.J., McIntyre P.;
RT      "Biochemical properties of rat protein kinase C-eta expressed in COS
RT      cells."
RL      FEBS Lett. 312:195-199(1992).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC      TISSUE=Lung;
RG      NIH - Mammalian Gene Collection (MGC) project;
RL      Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
CC      serine- and threonine-specific enzyme.
CC      -1- FUNCTION: PKC is activated by diacylglycerol which in turn
CC      phosphorylates a range of cellular proteins. PKC also serves as
CC      the receptor for phorbol esters, a class of tumor promoters.
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
CC      subfamily.
CC      -1- SIMILARITY: Contains 1 C2 domain.
CC      -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; X68400; CAA48466.1; -; mRNA.
DR      EMBL; BC081782; AAH81782.1; -; mRNA.
DR      PIR; I60246; S29478.
DR      HSSP; P28867; 1PTO.
DR      Ensembl; ENSRNOG00000004873; Rattus norvegicus.
DR      RGD; 621888; Prkch.
DR      GO; GO:0004672; F:protein kinase activity; IDA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR002219; DAG_PR_bd.
DR      InterPro; IPR000961; PKinase_C.
DR      InterPro; IPR000719; Prot_Kinase.
DR      InterPro; IPR008271; Ser_thr_pkin_AS.
DR      InterPro; IPR002290; Ser_thr_pkinase.
DR      Pfam; PF00130; C1.1; 2.
DR      Pfam; PF00168; C2.1.
DR      Pfam; PF00063; PKinase; 1.
DR      Pfam; PF00433; PKinase_C; 1.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00008; DAGDOMAIN.
DR      ProDom; PD000001; Prot_kinase; 1.

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DR      SMART; SM00109; C1; 2.
DR      SMART; SM00239; C2; 1.
DR      SMART; SM00133; S_TK_X; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50004; C2_DOMAIN; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      PROSITE; PS00479; ZF_DAG_PR_1; 2.
DR      PROSITE; PS50081; ZF_DAG_PR_2; 2.
DR      ATP-binding; Kinase; Metal-Binding; Nucleotide-binding;
DR      Phorbol-ester binding; Repeat; Serine/threonine-protein kinase;
KW      Transferase; Zinc; Zinc-finger.
FT      DOMAIN 12 102
FT      ZN_FING 355 614
FT      ZN_FING 171 222
FT      ZN_FING 245 295
FT      NP_BIND 361 369
FT      ACT_SITE 479 479
FT      BINDING 384 384
SQ      SEQUENCE 683 AA; 77947 MW; 2F5B7078D1206510 CRC64;

Query Match          79.2%; Score 38; DB 1; Length 683;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HDAPICVD 8
Db      88 HETPLGYD 95

RESULT 26
Q8NE03 HUMAN
ID      Q8NE03;
AC      Q8NE03;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Protein kinase C, eta.
GN      Name=PRKCH;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Testis;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Krausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Halel P.,
RA      Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udell T.B., Toobyki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., McWan P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butcherfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
RA      Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Testis;
RG      NIH MGC Project;

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CC Pteromalidae; Pteromalinae; Nasonia.  
 OX NCBI\_TaxID=7425;  
 [1]  
 RP NUCLEOTIDE SEQUENCE  
 RX BURKE=93196484; PubMed=8383793;  
 RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.,  
 RT "Sequence relationship of retrotransposable elements R1 and R2 within  
 and between divergent insect species.";  
 RL Mol. Biol. Evol. 10:163-185(1993).  
 [2]  
 RP SEQUENCE REVISION.  
 RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.,  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Deoxynucleoside triphosphate + DNA(n) =  
 diphosphate + DNA(n+1).  
 CC -1- SIMILARITY: Contains 1 C2H2-type zinc finger.  
 CC -1- SIMILARITY: Contains 1 reverse transcriptase domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR EMBL; L00950; AAC34927.1; -; Genomic\_DNA.  
 DR PIR; T10259; T10259.  
 DR InterPro; IPR000477; RVTse.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF00078; RVT\_1; 1.  
 DR SMART; SM00355; Znf\_C2H2; 1.  
 DR PROSITE; PS50878; RT\_POL; 1.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 1.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 1.  
 DR Endonuclease; Hydrolase; Metal-binding; Nuclease;  
 KM Nucleicacyltransferase; RNA-directed DNA polymerase; Transferase;  
 FT DOMAIN 358 635 Reverse transcriptase.  
 FT ZN FING 46 69 C2H2-type.  
 FT REGION 755 1025 Nucleic acid-binding endonuclease.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 1025 AA; 115885 MW; 387BDE63BCF5C518 CRC64;  
 Query March 79.2%; Score 38; DB 1; Length 1025;  
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HDAPIGY 7  
 Db 709 HDPIGV 715

RT "Complete genome sequence of the plant commensal Pseudomonas  
 RT fluorescens Pf-5.";  
 RL Nat. Biotechnol. 23:873-878(2005).  
 DR EMBL; CP000076; AA92727.1; -; Genomic\_DNA.  
 KM TRANSFERASE.  
 SQ SEQUENCE 379 AA; 43072 MW; FB8E37F559CAEF8A CRC64;  
 Query March 77.1%; Score 37; DB 2; Length 379;  
 Best Local Similarity 71.4%; Pred. No. 60;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HDAPIGY 7  
 Db 148 HDAPVGR 154

RESULT 30  
 044320 HIPCN  
 ID 044320 HIPCN PRELIMINARY; PRT; 493 AA.  
 AC 044320;  
 DT 01-JUN-1998 (TReMBLrel. 06, Created)  
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Reverse transcriptase (Fragment).  
 GN Name=R2 ORF;  
 OS Hippodamia convergens (Convergent lady beetle).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Coccinellidae; Coccinellinae; Coccinellini; Hippodamia.  
 OX NCBI\_TaxID=64696;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Burke W.D., Malik H.S., Eickbush T.H.,  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF015816; AA894040.1; -; Genomic\_DNA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.  
 KM RNA-directed DNA polymerase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 493 AA; 55882 MW; 9E776B92C636B9C9 CRC64;  
 Query March 77.1%; Score 37; DB 2; Length 493;  
 Best Local Similarity 71.4%; Pred. No. 80;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HDAPIGY 7  
 Db 159 HDVPGV 165

RESULT 31  
 04PGX8 USTWA  
 ID 04PGX8 USTWA PRELIMINARY; PRT; 685 AA.  
 AC 04PGX8;  
 DT 13-SEP-2005 (TReMBLrel. 31, Created)  
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=UM00635.1;  
 OS Ustilago maydis 521.  
 OC Basidiomycota; Basidiomycetes; Ustilaginomycetes;  
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 OX NCBI\_TaxID=237631;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Birren B., Nuebaum C., Abebe A., Abouelleil A., Adekoya E.,  
 RA Alt-zehra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
 RA Aarachi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,  
 RA Bayul T., Biltstein B., Bloom T., Bye J., Boguslavsky L.,  
 RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,

RA Calvo S., Camarata J., Campo K., Chang J., Cheeshaens Y., Citroen M.,  
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
RA David L., Dawe T., Degray S., Dodge S., Dooley P., Dorje P.,  
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gierre S.,  
RA Gintke A., Goyette A., Graham J., Grandbois E., Gyalsen K., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
RA Hagan T., Horn A., Houde N., Hughes L., Hulme W., Hubby E., Iliev I.,  
RA Jaffe D., Jones C., Kamel M., Kamat A., Kamysellis M., Karlsson E.,  
RA Kells C., Kieu A., Kisser P., Kodira C., Kulbokas E., Labutis K.,  
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
RA Lindblad-coh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,  
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
RA McCarthy M., McDonough S., McGhee T., Meldrum J., Meneus L.,  
RA Mestrov J., Mihalev A., Minova T., Mikkelsen T., Mlenga V., Moru K.,  
RA Moses J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,  
RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotohio B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquant B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
RA Ratta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Shtinov S., Smith C., Sougnaz C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stetson K., Stone C., Stone S., Stubbs M., Talama J., Tehunga P.,  
RA Tenzing P., Teste S., Theodore J., Thoulusang Y., Topham K.,  
RA Toney S., Tsamla T., Tecmo N., Vallee D., Vassiliou H.,  
RA Venkateraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadev S.,  
RA Yang S., Yang X., Yeager S., Yee B., Young G., Zainoun J., Zembeck L.,  
RA Zimmer A., Zody M., Lander E.;  
RT "The genome sequence of *Ustilago maydis*.";  
RL Submitted (FEB-2004) to the EMBL/Genbank/DDBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; AACP01000015; EAK01064.1; -; Genomic\_DNA.  
DR Hypothetical protein.  
KM  
SQ SEQUENCE 685 AA; 74135 MW; BD622893463B10E2 CRC64;

Query Match 77.1%; Score 37; DB 2; Length 685;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPGVY 7  
DB 269 HEAPGVY 275  
  
RESULT 32  
O91WX8.RAT PRELIMINARY; PRT; 695 AA.  
AC O91WX8;  
DT 01-DEC-2001 (TRENBLREL. 19, Created)  
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
DE Voltage-gated calcium channel pore forming subunit Cav1.3alpha1  
DE (Fragment).  
OS *Rattus norvegicus* (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eultheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
OX [1]  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN-Sprengue-Dawley; TISSUE=superior cervical ganglia;  
RX MEDLINE=21380268; PubMed=11487617;  
RX Xu W., Lipscombe D.;  
RT "Neuronal Ca(V)1.3alpha(1) L-type channels activate at relatively  
RT hyperpolarized membrane potentials and are incompletely inhibited by  
RT dihydropyridines.";

RL J. Neurosci. 21:5944-5951(2001).  
DR EMBL; AF370010; AA072960.1; -; mRNA.  
DR EMBL; ENSRNOG0000013147; Rattus norvegicus.  
FT NON TER 1  
SQ SEQUENCE 695 AA; 79033 MW; B9A5A1CE11FB7D32 CRC64;  
  
Query Match 77.1%; Score 37; DB 2; Length 695;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGYD 8  
DB 429 DSPIGYD 435  
  
RESULT 33  
CACID.RAT STANDARD; PRT; 2203 AA.  
AC P27732; O09022; O09023; O01542; Q62691; Q62815; Q63491;  
AC Q63492;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Voltage-  
DE gated calcium channel alpha subunit Cav1.3) (Calcium channel, L type,  
DE alpha-1 polypeptide, isoform 2) (Rat brain class D) (RBD).  
GN Name=Cacal1d; Synonyms=Cacch3, Cacn4, Cacn1a2, Cch11a2;  
OS *Rattus norvegicus* (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eultheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).  
RC TISSUE=Insulinoma;  
RX MEDLINE=95280950; PubMed=7760845; DOI=10.1210/me.9.1.121;  
RX Ihara Y., Yamada Y., Fujii Y., Gonoi T., Yano H., Yasuda K.,  
RX Inagaki N., Saito Y., Saito S.;  
RT "Molecular diversity and functional characterization of voltage-  
RT dependent calcium channels (CACN4) expressed in pancreatic beta-  
RT cells.";  
RL Mol. Endocrinol. 9:121-130(1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS 3, 6, 7, 8 AND 13).  
RC TISSUE=Brain;  
RX MEDLINE=91299338; PubMed=1648940; DOI=10.1016/0896-6273(91)90072-8;  
RX Hui A., Billnor P.T., Krizanov O., Wang J.-J., Diebold R.J.,  
RX Schwartz A.;  
RT "Molecular cloning of multiple subtypes of a novel rat brain isoform  
RT of the alpha-1 subunit of the voltage-dependent calcium channel.";  
RL Neuron 7:35-44(1991).  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 1-125.  
RX MEDLINE=96040125; PubMed=7553731;  
RX Kamp T.J., Milas M., Fields K.L., Aesch S., Chin H., Marban E.,  
RX Nirenberg M.;  
RT "Transcriptional regulation of the neuronal L-type calcium channel  
RT alpha 1D subunit gene.";  
RL Cell. Mol. Neurobiol. 15:307-326(1995).  
RN [4]  
RP NUCLEOTIDE SEQUENCE OF 1100-1410 (ISOFORMS 4 AND 11).  
RC TISSUE=Kidney;  
RX MEDLINE=93066265; PubMed=1279681;  
RX Yu A.S.L., Hebert S.C., Brenner B.M., Lytton J.;  
RT "Molecular characterization and nephron distribution of a family of  
RT transcripts encoding the pore-forming subunit of Ca2+ channels in the  
RT kidney.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498(1992).  
RN [5]  
RP NUCLEOTIDE SEQUENCE OF 1218-1498 (ISOFORM 12).  
RC TISSUE=Osteocarcinoma;  
RX MEDLINE=96074617; PubMed=7479909;  
RX Barry E.L.R., Geesek F.A., Froehner S.C., Friedman P.A.;

RT "Multiple calcium channel transcripts in rat osteosarcoma cells:  
RT selective activation of alpha 1D isoform by parathyroid hormone.";  
RT Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).  
RN [6]  
RP NUCLEOTIDE SEQUENCE OF 1200-1493 (ISOFORMS 3; 4; 5; 9 AND 10).  
RC TISSUE=Hepatoma;  
RX MEDLINE=97376179; PubMed=9232351; DOI=10.1016/S0143-4160(97)90088-9;  
RA Breerem H.M., Harland M.L., Froscio M., Petronijevic T.,  
RA Barrett G.J.;  
RT "Novel variants of voltage-operated calcium channel alpha-1 subunit  
RT transcripts in a rat liver-derived cell line: deletion in the IVS4  
RT voltage sensing region.";  
RT Cell Calcium 22:39-52(1997).  
RN [7]  
RP NUCLEOTIDE SEQUENCE OF 1307-1479 (ISOFORM 3).  
RX MEDLINE=90239020; PubMed=1692134;  
RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.,  
RT "Rat brain expresses a heterogeneous family of calcium channels.";  
RT Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).  
CC -1- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the  
CC entry of calcium ions into excitable cells and are also involved  
CC in a variety of calcium-dependent processes, including muscle  
CC contraction, hormone or neurotransmitter release, gene expression,  
CC cell motility, cell division and cell death. The isoform alpha-1D  
CC gives rise to L-type calcium currents. Long-lasting (L-type)  
CC calcium channels belong to the "high-voltage activated" (HVA)  
CC group. They are blocked by dihydropyridines (DHP),  
CC phenylalkylamines, benzothiazepines, and by omega-agatoxin-IIIa  
CC (omega-Aga-IIIa). They are however insensitive to omega-conotoxin-  
CC GVIA (omega-CTX-GVIA) and omega-agatoxin-IVA (omega-Aga-IVA).  
CC -1- SUBUNIT: Voltage-dependent calcium channels are multisubunit  
CC complexes, consisting of alpha-1, alpha-2, beta and delta subunits  
CC in a 1:1:1:1 ratio. The channel activity is directed by the pore-  
CC forming and voltage-sensitive alpha-1 subunit. In many cases, this  
CC subunit is sufficient to generate voltage-sensitive calcium  
CC channel activity. The auxiliary subunits beta and alpha-2/delta  
CC linked by a disulfide bridge regulate the channel activity.  
CC Interacts with RIMBP2 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=13;  
CC Comment=The region sequenced in isoforms ROB3 and RKC5 is  
CC identical to CACNA4;  
CC Name=1; Synonym=CACNA4;  
CC IsoId=P27732-1; Sequence=Displayed;  
CC Name=2; Synonym=CACNA4B;  
CC IsoId=P27732-2; Sequence=VSP\_000923; VSP\_000924;  
CC Name=3; Synonym=CACNA3, RB48, RBD-55;  
CC IsoId=P27732-3; Sequence=VSP\_000921;  
CC Name=4; Synonym=Delta-IV-S3, RKC6;  
CC IsoId=P27732-4; Sequence=VSP\_000919;  
CC Name=5; Synonym=Delta-IV-S4;  
CC IsoId=P27732-5; Sequence=VSP\_000922;  
CC Name=6; Synonym=RB9;  
CC IsoId=P27732-6; Sequence=VSP\_000920, VSP\_000921;  
CC Name=7; Synonym=RB11;  
CC IsoId=P27732-7; Sequence=VSP\_000917;  
CC Name=8; Synonym=RB34;  
CC IsoId=P27732-8; Sequence=VSP\_000916;  
CC Name=9; Synonym=RH1;  
CC IsoId=P27732-9; Sequence=VSP\_000918;  
CC Name=10; Synonym=RH2;  
CC IsoId=P27732-10; Sequence=VSP\_000919, VSP\_000922;  
CC Name=11; Synonym=RKC5;  
CC IsoId=P27732-13; Sequence=Not described;  
CC Name=12; Synonym=ROB3;  
CC IsoId=P27732-14; Sequence=Not described;  
CC Name=13; Synonym=Truncated;  
CC IsoId=P27732-12; Sequence=VSP\_000925, VSP\_000926;  
CC -1- TISSUE SPECIFICITY: Expressed in brain, pancreatic islets and B-  
CC lymphocytes.  
CC -1- DOMAIN: Each of the four internal repeats contains five  
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one

CC positively charged transmembrane segment (S4). S4 segments  
CC probably represent the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunit family.  
CC -----  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; D38101; BAA07282.1; -; mRNA.  
DR EMBL; D38102; BAA07283.1; -; mRNA.  
DR EMBL; M57682; AAA42015.1; -; mRNA.  
DR EMBL; U14005; AAB60515.1; -; Genomic\_DNA.  
DR EMBL; M99221; AAA40895.1; -; mRNA.  
DR EMBL; U31772; AAB89156.1; -; mRNA.  
DR EMBL; U49126; AAB61634.1; -; mRNA.  
DR EMBL; U49127; AAB61635.1; -; mRNA.  
DR EMBL; U49128; AAB61636.1; -; mRNA.  
DR Ensemble; ENSRNOG00000013147; Rattus norvegicus.  
DR RGD; 70973; Cacaatd.  
DR GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.  
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.  
DR GO; GO:0019722; P:calcium-mediated signalling; IDA.  
DR InterPro; IPR001682; Ca/Na pore.  
DR InterPro; IPR002077; Ca channel alpha.  
DR InterPro; IPR002111; Cat\_channel\_TFPL.  
DR InterPro; IPR0011992; EF-Hand type.  
DR InterPro; IPR005821; Ion trans.  
DR InterPro; IPR003091; K channel.  
DR InterPro; IPR005446; LVDCCALpha1.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR00167; KCHANNEL.  
DR PRINTS; PR00169; KCHANNEL.  
DR PRINTS; PR01630; LVDCCALPHA1.  
DR PRINTS; PR01636; LVDCCALPHA1D.  
KW Alternative splicing; Calcium; Calcium channel; Calcium transport;  
KW Glycoprotein; Ion transport; Ionic channel; Multigene family;  
KW Phosphorylation; Repeat; Transmembrane; Transport;  
KW Voltage-gated channel.  
FT TOPO\_DOM 1 126  
FT TRANSMEM 127 145  
FT TOPO\_DOM 146 163  
FT TRANSMEM 164 183  
FT TOPO\_DOM 184 195  
FT TRANSMEM 196 214  
FT TOPO\_DOM 215 235  
FT TRANSMEM 236 254  
FT TOPO\_DOM 255 273  
FT TRANSMEM 274 293  
FT TOPO\_DOM 294 381  
FT TRANSMEM 382 406  
FT TOPO\_DOM 407 582  
FT TRANSMEM 583 602  
FT TOPO\_DOM 603 617  
FT TRANSMEM 618 636  
FT TOPO\_DOM 637 644  
FT TRANSMEM 645 663  
FT TOPO\_DOM 664 673  
FT TRANSMEM 674 692  
FT TOPO\_DOM 693 711  
FT TRANSMEM 712 732  
FT TOPO\_DOM 733 786  
FT TRANSMEM 787 811  
FT TOPO\_DOM 812 945  
FT TRANSMEM 946 964  
FT TOPO\_DOM 965 980  
FT TRANSMEM 981 1000  
Query Match 77.1%; Score 37; DB 1; Length 2203;

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Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 1937 DSPIGYD 1943

RESULT 34
Q6D7L9 ERWCT PRELIMINARY; PRT; 213 AA.
ID Q6D7L9 ERWCT PRELIMINARY; PRT; 213 AA.
AC Q6D7L9 ERWCT PRELIMINARY; PRT; 213 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Nicotinate-nucleotide adenyllyltransferase (Conserved hypothetical
protein) (EC 2.7.7.18).
GN Name=nadD; OrderedLocustNames=BCA1306;
OS Erwiniia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.040242101;
RA Bell K.S., Sepahnia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holava M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Altin R., Bason N., Brooks K., Chillingworth T., Clark K., Dougett J.,
RA Fraser A., Hance Z., Hauser H., Jørgensen K., Moulie S., Norberg-Knudsen H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.V., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwiniia
carotovora subsp. atroseptica and characterization of virulence
factors."
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
RU EMBL; BX950851; CNG74216.1; -; Genomic DNA.
DR GO; GO:0004515; F:nicotinate-nucleotide adenyllyltransferase a. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0009435; P:NAD biosynthesis; IEA.
DR InterPro; IPR004820; Cytidylyltransf.
DR InterPro; IPR004821; Cytidylyltransf.
DR InterPro; IPR005248; NAMN_adtnstrase.
DR Pfam; PF01467; CTP_transf.2; 1.
DR TIGRFAMs; TIGR00125; cyt_tran_rel.1.
DR TIGRFAMs; TIGR00482; NAMN_adtnstrase; 1.
KW Complete proteome; Hypothetical protein; Nucleotidyltransferase;
KW Transferrase.
SQ SEQUENCE 213 AA; 24208 MW; C7C3DBFF68941B9C CRC64;

Query Match 75.0%; Score 36; DB 2; Length 213;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPGYD 7
Db 98 HDAPLGF 104

RESULT 35
Q8UJ40 XENLA PRELIMINARY; PRT; 229 AA.
ID Q8UJ40 XENLA PRELIMINARY; PRT; 229 AA.
AC Q8UJ40;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
DE Mitotic phosphoprotein 77 (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21676254; PubMed=11818060; DOI=10.1016/S0960-9822(01)00662-5;
RA Georgi A.B., Stukenberg P.T., Kirschner M.W.;
RT "Timing of events in mitosis."
RL Curr. Biol. 12:1105-1114(2002).
DR EMBL; AF419154; AM33249.1; -; mRNA.
DR HSSP; P00740; ICFH.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VltR_dep_GLA.
DR Pfam; PF00594; GLA; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS50998; GLA_2; 1.
FT NON TER 229
SQ SEQUENCE 229 AA; 25543 MW; 42A2856B9A6A6A9 CRC64;

Query Match 75.0%; Score 36; DB 2; Length 229;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 157 DSPVGYD 163

RESULT 36
Q4PDF5 USTMA PRELIMINARY; PRT; 461 AA.
ID Q4PDF5 USTMA PRELIMINARY; PRT; 461 AA.
AC Q4PDF5;
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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OM01858.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Aliz-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Amburster J., Bachanteng P., Baldwin C., Barry A.,
RA Bayul T., Biltshetyn B., Bloom T., Blye J., Boguslavsky L.,
RA Botovsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheeshaeng Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geartn G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyalsen K., Hafez N.,
RA Hagopian D., Hagoos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Hueb E., Iliev I.,
RA Jaffe D., Jones C., Kamel M., Kamet A., Kanyasels M., Karlsson E.,
RA Kells C., Kieu A., Kistner P., Kodira C., Kulbokas E., Labucci K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-Toh K., Liu X., Lokysiang T., Lokysiang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabelli R., Maru K., Matthews C., Mauceli B.,
RA McCarthy M., McDonough S., McGhee T., Meldrum J., Menais V.,
RA Mesirov J., Mihalev A., Minova T., Mikkelsen T., Mlenga V., Moru K.,
RA Moses J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizati M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotoesho B.,
RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Piquant B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,

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RA Rutman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,  
 RA Sheridan J., Shepa N., Shi J., Smirnov S., Smith C., Sougnuez C.,  
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
 RA Steuson K., Stone C., Stone S., Stubbs M., Talamao U., Tchinga P.,  
 RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,  
 RA Toney S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,  
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Mangchuk T.,  
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wymann D., Yadav S.,  
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
 RA Zimmer A., Zody M., Lander E.;  
 RT "The genome sequence of *Ustilago maydis*.";  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC preliminary data  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 DR EMBL; AAC0100070; EAK82739.1; -; Genomic\_DNA.  
 DR InterPro; IPR005925; Agmatinase.  
 DR InterPro; IPR006035; Arg agm form.  
 DR InterPro; IPR005924; Arginase.  
 DR Pfam; PF00491; Arginase; 1.  
 DR PRINTS; PR00116; ARGINASE.  
 DR TIGRFAMs; TIGR01230; agmatinase; 1.  
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Qy 1 HDAPIGD 8  
 Db 312 HDASIGFD 319

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 DT 25-OCT-2004 (TREMBlrel. 28; Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28; Last annotation update)  
 DE Hypothetical protein OSCNB0058118.37.  
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 OS Oryza sativa (Japonica cultivar-group).  
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 OC NCBI\_TaxID=39947;  
 RX NCBI\_TaxID=39947;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Katayose Y.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC  
 RT clone:OSUNBA0058118.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP005125; BAD30915.1; -; Genomic\_DNA.  
 DR Gramene; Q69S31; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 66 AA; 6970 MW; 48F4CA89A983ECD6 CRC64;

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Qy 1 HDAPIG 6  
 Db 13 HDAPIG 18

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ID Q9FSF3\_AGRRH PRELIMINARY; PRT; 171 AA.  
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 DT 01-MAR-2001 (TREMBlrel. 16; Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24; Last annotation update)  
 DE Riorf97 protein.  
 GN Name=riorf97;  
 OS Agrobacterium rhizogenes.  
 OC plasmid pRi1724.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
 OC NCBI\_TaxID=359;  
 RX NCBI\_TaxID=359;  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MAFP03-01724;  
 RA Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;  
 RT "Genome structure of R1 plasmid (1): Construction of linking library  
 RT and physical map of pRi1724 in Japanese Agrobacterium.";  
 RL Nucleic Acids Symp. Ser. 39:189-190(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MAFP03-01724;  
 RA Maeda Y., Moriguchi K., Kataoka M., Satou M., Satou N., Tanaka N.,  
 RA Yoshida K.;  
 RT "Genome structure of R1 plasmid (1): Sequencing analysis of T-DNA and  
 RT its flanking regions of pRi1724 in Japanese Agrobacterium  
 RT rhizogenes.";  
 RL Nucleic Acids Symp. Ser. 42:67-68(1999).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MAFP03-01724;  
 RX PubMed=11273700; DOI=10.1006/jmbi.2001.4488;  
 RA Moriguchi K., Maeda Y., Satou M., Hardayani N.S.N., Kataoka M.,  
 RA Tanaka N., Yoshida K.;  
 RT "The complete nucleotide sequence of a plant root-inducing (Ri)  
 RT plasmid indicates its chimeric structure and evolutionary relationship  
 RT between tumor-inducing (Ti) and symbiotic (Sym) plasmids in  
 RT Rhizobiaceae.";  
 RL J. Mol. Biol. 307:771-784(2001).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MAFP03-01724;  
 RX MEDLINE=20363091; PubMed=10907845;  
 RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;  
 RT "Analysis of unique variable region of a plant root inducing plasmid,  
 RT pRi1724, by the construction of its physical map and library.";  
 RL DNA Res. 7:157-163(2000).  
 DR EMBL; AP002086; BAB16216.1; -; Genomic\_DNA.  
 KW Plasmid.  
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 AC Q9LZG9;  
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 DT 01-OCT-2000 (TREMBlrel. 15; Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)  
 DE Hypothetical protein T28A8\_70.  
 GN Name=T28A8\_70;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Punnett B., Boutry M., Goffeau A., Mewes H.W., Rudd S., Lemcke K.,
RA Mayer K.F.X., Queffier F., Salanoubat M.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL162691; CAB83150.1; -; Genomic_DNA.
DR PIR; T47414; T47414.
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DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
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GN Name=tlorf60;
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFP301001;
RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (I): Strategy for DNA sequencing of a
RT Japanese cherry-Ti plasmid."
RL Nucleic Acids Symp. Ser. 37:159-160(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFP301001;
RA Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (III): Characteristics of T-DNA."
RL Nucleic Acids Symp. Ser. 39:185-186(1998).
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RC STRAIN=MAFP301001;
RA Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (IV): Characteristics of tra region."
RL Nucleic Acids Symp. Ser. 39:187-188(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFP301001;
RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (V): Complete nucleotide sequence of
RT plasmid pTI-SAKURA's vir region in Agrobacterium tumefaciens."
RL Nucleic Acids Symp. Ser. 39:265-266(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFP301001;
RX MEDLINE=20184752; PubMed=10721727; DOI=10.1016/S0378-1119(99)00502-8;
RA Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
RA Katoh A., Yoshida K.;
RT "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid."
RL Gene 242:331-336(2000).
RN [6]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFP301001;
RX MEDLINE=98193120; PubMed=9524202; DOI=10.1016/S0167-4781(97)00182-6;
RA Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT "Novel structural difference between nopaline- and octopine- type trbu
RT gene: construction of genetic and physical map and sequencing of
RT trb/traI and rep gene clusters of a new Ti plasmid pTI-SAKURA."
RL Blochim. Biophys. Acta 1396:1-7(1998).
DR EMBL; AB016260; BAA87685.1; -; Genomic_DNA.
KM Plasmid.
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Query Match
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Oy 2 DAPIGYD 8
Db 127 DGPVGYD 133

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Search completed: December 3, 2005, 23:42:54  
Job time : 232 secs



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpn** and **.rnpn**. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapn** and **.rapn**.

***Because they contain data that is confidential, the results of Pending database searches should not be left in the case .***

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Curison k.  
10/807553 Page 3  
Seq. ID 2 w/ notes

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:24:59 ; Search time 567 Seconds

(without alignments)  
19.498 Million cell updates/sec

Title: US-10-807-553-2  
Perfect score: 48  
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Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 761189 seqs, 1381955077 residues  
Total number of hits satisfying chosen parameters: 761189

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Pending Patents AA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	48	100.0	8	30 US-10-007-363-2	Sequence 2, Appl1
4	48	100.0	8	38 US-10-807-553-2	Sequence 2, Appl1
5	48	100.0	8	40 US-11-011-557-3	Sequence 3, Appl1
6	48	100.0	30	40 US-11-011-557-93	Sequence 93, Appl1
7	48	100.0	123	46 US-60-208-965-244	Sequence 244, Appl1
8	48	100.0	125	46 US-60-233-606-114	Sequence 114, Appl1
9	48	100.0	231	39 US-10-932-349-1539	Sequence 1539, Appl1
10	48	100.0	231	49 US-60-500-337-1539	Sequence 1539, Appl1
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54	48	100.0	737	27 US-09-724-676A-68820	Sequence 68820, Appl1
55	48	100.0	737	27 US-09-724-676A-68820	Sequence 68820, Appl1

56	44	91.7	8	1	PCT-US02-11754-7	Sequence 7, Appl1
57	44	91.7	8	1	PCT-US02-11754-13	Sequence 13, Appl1
58	44	91.7	8	30	US-10-007-363-7	Sequence 7, Appl1
59	44	91.7	8	30	US-10-007-363-13	Sequence 13, Appl1
60	44	91.7	8	38	US-10-807-553-7	Sequence 7, Appl1
61	44	91.7	8	38	US-10-807-553-13	Sequence 13, Appl1
62	44	91.7	8	40	US-11-011-557-9	Sequence 9, Appl1
63	44	91.7	8	40	US-11-011-557-15	Sequence 15, Appl1
64	44	91.7	8	40	US-11-011-557-31	Sequence 31, Appl1
65	43	89.6	8	1	PCT-US01-51600-8	Sequence 8, Appl1
66	43	89.6	8	30	US-10-007-363-8	Sequence 8, Appl1
67	43	89.6	8	38	US-10-807-553-8	Sequence 8, Appl1
68	43	89.6	8	40	US-11-011-557-10	Sequence 10, Appl1
69	43	89.6	8	40	US-11-011-557-55	Sequence 55, Appl1
70	43	89.6	8	1	PCT-US01-51600-9	Sequence 9, Appl1
71	42	87.5	8	1	PCT-US02-11754-9	Sequence 9, Appl1
72	42	87.5	8	30	US-10-007-363-9	Sequence 9, Appl1
73	42	87.5	8	38	US-10-807-553-9	Sequence 9, Appl1
74	42	87.5	8	40	US-11-011-557-11	Sequence 11, Appl1
75	42	87.5	8	40	US-11-011-557-29	Sequence 29, Appl1
76	42	87.5	8	1	PCT-US01-51600-12	Sequence 12, Appl1
77	40	83.3	8	1	PCT-US01-51600-14	Sequence 14, Appl1
78	40	83.3	8	1	PCT-US02-11754-12	Sequence 12, Appl1
79	40	83.3	8	1	PCT-US02-11754-14	Sequence 14, Appl1
80	40	83.3	8	30	US-10-007-363-12	Sequence 12, Appl1
81	40	83.3	8	30	US-10-007-363-14	Sequence 14, Appl1
82	40	83.3	8	38	US-10-807-553-12	Sequence 12, Appl1
83	40	83.3	8	38	US-10-807-553-14	Sequence 14, Appl1
84	40	83.3	8	40	US-11-011-557-14	Sequence 14, Appl1
85	40	83.3	8	40	US-11-011-557-16	Sequence 16, Appl1
86	40	83.3	8	40	US-11-011-557-21	Sequence 21, Appl1
87	40	83.3	8	40	US-11-011-557-79	Sequence 79, Appl1
88	40	83.3	8	40	US-10-437-963-131067	Sequence 131067, Appl1
89	39	81.2	719	31	US-10-155-881-29363	Sequence 29363, A
90	39	81.2	719	34	US-10-437-963-172827	Sequence 172827, A
91	39	81.2	719	34	US-10-438-246-18373	Sequence 18373, A
92	39	81.2	719	34	US-10-438-246-25324	Sequence 25324, A
93	39	81.2	719	27	US-09-791-537-35217	Sequence 35217, A
94	39	81.2	719	27	US-09-791-537-35217	Sequence 35217, A
95	38	79.2	18	40	US-11-011-557-6	Sequence 6, Appl1
96	38	79.2	18	40	US-11-011-557-96	Sequence 96, Appl1
97	38	79.2	35	1	PCT-US02-22868-290	Sequence 290, App
98	38	79.2	35	1	US-10-199-820-290	Sequence 290, App
99	38	79.2	91	45	US-60-160-209-2783	Sequence 2783, Ap
100	38	79.2	116	45	US-60-169-868-6771	Sequence 6771, Ap

## ALIGNMENTS

RESULT 1  
PCT-US01-51600-2  
Sequence 2, Application PC/TUS0151600  
GENERAL INFORMATION:  
APPLICANT: The Board of Trustees of the Leland  
APPLICANT: Stanford Junior University  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
TITLE OF INVENTION: Ischemia  
FILE REFERENCE: 58600-8209.WO00  
CURRENT APPLICATION NUMBER: PCT/US01/51600  
CURRENT FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pseudo-epsilon RACK octapeptide  
PCT-US01-51600-2

Query Match 100.0%; Score 48; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8  
DB 1 HDAPIGYD 8

RESULT 2  
PCT-US02-11754-2  
Sequence 2, Application PC/TUS0211754  
GENERAL INFORMATION:  
APPLICANT: The Board of Trustees of the Leland  
APPLICANT: Stanford Junior University  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
TITLE OF INVENTION: Ischemia  
FILE REFERENCE: 58600-8209.WO00  
CURRENT APPLICATION NUMBER: PCT/US02/11754  
CURRENT FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pseudo-epsilon RACK octapeptide  
PCT-US02-11754-2

Query Match 100.0%; Score 48; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8  
DB 1 HDAPIGYD 8

RESULT 3  
US-10-007-363-2  
Sequence 2, Application US/10007363  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
TITLE OF INVENTION: Ischemia  
FILE REFERENCE: 58600-8209.US00  
CURRENT APPLICATION NUMBER: US/10/007,363  
CURRENT FILING DATE: 2002-11-09  
PRIOR APPLICATION NUMBER: US 60/247,830  
PRIOR FILING DATE: 2000-11-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pseudo-epsilon RACK octapeptide  
US-10-007-363-2

ABN

Query Match 100.0%; Score 48; DB 30; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8  
DB 1 HDAPIGYD 8

RESULT 4  
US-10-807-553-2  
; Sequence 2, Application US/10807553  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition  
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to  
; TITLE OF INVENTION: Ischemia  
; FILE REFERENCE: 58600-8209.US00  
; CURRENT APPLICATION NUMBER: US/10/807,553  
; CURRENT FILING DATE: 2004-03-22  
; PRIOR APPLICATION NUMBER: US/10/007,363  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: US 60/247,830  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pseudo-epsilon RACK octapeptide  
US-10-807-553-2

Query Match  
Best Local Similarity 100.0%; Score 48; DB 38; Length 8;  
Pred. No. 7.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 5  
US-11-011-557-3  
; Sequence 3, Application US/11011557  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Chen, Leon E.  
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
; FILE REFERENCE: 58600-8212.US00  
; CURRENT APPLICATION NUMBER: US/11/011,557  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: 60/529,223  
; PRIOR FILING DATE: 2003-12-11  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-011-557-3

Query Match  
Best Local Similarity 100.0%; Score 48; DB 40; Length 8;  
Pred. No. 7.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 6  
US-11-011-557-93  
; Sequence 93, Application US/11011557  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Chen, Leon E.  
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C  
; FILE REFERENCE: 58600-8212.US00

; CURRENT APPLICATION NUMBER: US/11/011,557  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: 60/529,223  
; PRIOR FILING DATE: 2003-12-11  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 93  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-011-557-93

Query Match  
Best Local Similarity 100.0%; Score 48; DB 40; Length 30;  
Pred. No. 0.35;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 15 HDAPIGYD 22

RESULT 7  
US-60-208-965-244  
; Sequence 244, Application US/60208965  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE  
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES  
; FILE REFERENCE: CL000639  
; CURRENT APPLICATION NUMBER: US/60/208,965  
; CURRENT FILING DATE: 2000-06-02  
; NUMBER OF SEQ ID NOS: 244  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 244  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-208-965-244

Query Match  
Best Local Similarity 100.0%; Score 48; DB 46; Length 123;  
Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 84 HDAPIGYD 91

RESULT 8  
US-60-233-606-114  
; Sequence 114, Application US/60233606  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE  
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES  
; FILE REFERENCE: CL000821  
; CURRENT APPLICATION NUMBER: US/60/233,606  
; CURRENT FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 114  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-233-606-114

Query Match  
Best Local Similarity 100.0%; Score 48; DB 46; Length 125;  
Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8

Db 71 HDAPIGYD 78

RESULT 9  
US-10-932-349-1539

/ Sequence 1539, Application US/10932349  
/ GENERAL INFORMATION:  
/ APPLICANT: CARGILL, Michele  
/ TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
/ TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND  
/ FILE REFERENCE: CLO01483  
/ CURRENT APPLICATION NUMBER: US/10/932,349  
/ CURRENT FILING DATE: 2004-09-02  
/ NUMBER OF SEQ ID NOS: 123188  
/ SOFTWARE: FASTSEQ for Windows Version 4.0  
/ SEQ ID NO: 1539  
/ LENGTH: 231  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-932-349-1539

Query Match 100.0%; Score 48; DB 39; Length 231;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 10  
US-60-500-337-1539

/ Sequence 1539, Application US/60500337  
/ GENERAL INFORMATION:  
/ APPLICANT: CARGILL, Michele  
/ TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
/ TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND  
/ FILE REFERENCE: CLO01483  
/ CURRENT APPLICATION NUMBER: US/60/500,337  
/ CURRENT FILING DATE: 2003-09-05  
/ NUMBER OF SEQ ID NOS: 123188  
/ SOFTWARE: FASTSEQ for Windows Version 4.0  
/ SEQ ID NO: 1539  
/ LENGTH: 231  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-60-500-337-1539

Query Match 100.0%; Score 48; DB 49; Length 231;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 11  
US-09-791-537-106215

/ Sequence 106215, Application US/09791537  
/ GENERAL INFORMATION:  
/ APPLICANT: Biomomix, Inc.  
/ APPLICANT: Debe, Derek  
/ APPLICANT: Danzer, Joseph  
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
/ FILE REFERENCE: 261/210  
/ CURRENT APPLICATION NUMBER: US/09/791,537  
/ CURRENT FILING DATE: 2001-02-22  
/ NUMBER OF SEQ ID NOS: 153055

/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO: 106215  
/ LENGTH: 736  
/ TYPE: PRT  
/ ORGANISM: Oryctolagus cuniculus  
US-09-791-537-106215

Query Match 100.0%; Score 48; DB 27; Length 736;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 12  
US-09-791-537-108607

/ Sequence 108607, Application US/09791537  
/ GENERAL INFORMATION:  
/ APPLICANT: Biomomix, Inc.  
/ APPLICANT: Debe, Derek  
/ APPLICANT: Danzer, Joseph  
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
/ FILE REFERENCE: 261/210  
/ CURRENT APPLICATION NUMBER: US/09/791,537  
/ CURRENT FILING DATE: 2001-02-22  
/ NUMBER OF SEQ ID NOS: 153055  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO: 108607  
/ LENGTH: 736  
/ TYPE: PRT  
/ ORGANISM: Oryctolagus cuniculus  
US-09-791-537-108607

Query Match 100.0%; Score 48; DB 27; Length 736;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 13  
PCT-US02-01048-2

/ Sequence 2, Application PC/TUS0201048  
/ GENERAL INFORMATION:  
/ APPLICANT: EXLIXIS, INC.  
/ TITLE OF INVENTION: Modulating Insulin Receptor Signaling  
/ FILE REFERENCE: EX02-001C-PC  
/ CURRENT APPLICATION NUMBER: PCT/US02/01048  
/ CURRENT FILING DATE: 2002-01-11  
/ Prior Application removed - See File Wrapper or Palm  
/ NUMBER OF SEQ ID NOS: 76  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO: 2  
/ LENGTH: 737  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
PCT-US02-01048-2

Query Match 100.0%; Score 48; DB 1; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 85 HDAPIGYD 92

RESULT 14

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US-07-821-714-2
: Sequence 2, Application US/07821714
: GENERAL INFORMATION:
: APPLICANT: Basta, Patricia V.
: APPLICANT: Burns, David J.
: TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
: STREET: 1 Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/821,714
: FILING DATE: 19920114
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Hohenschutz, Liza D.
: REGISTRATION NUMBER: 33,712
: REFERENCE/DOCKET NUMBER: SPNX-0010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 737 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-821-714-2

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Query Match      100.0%; Score 48; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HDAPIGYD 8
Db      85 HDAPIGYD 92

```

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RESULT 15
US-07-821-714-4
: Sequence 4, Application US/07821714
: GENERAL INFORMATION:
: APPLICANT: Basta, Patricia V.
: APPLICANT: Burns, David J.
: TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
: STREET: 1 Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/821,714
: FILING DATE: 19920114
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Hohenschutz, Liza D.

```

```

: REGISTRATION NUMBER: 33,712
: REFERENCE/DOCKET NUMBER: SPNX-0010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 737 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-821-714-4

```

```

Query Match      100.0%; Score 48; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HDAPIGYD 8
Db      85 HDAPIGYD 92

```

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RESULT 16
US-08-087-341-2
: Sequence 2, Application US/08087341
: GENERAL INFORMATION:
: APPLICANT: Basta, Patricia V.
: APPLICANT: Burns, David J.
: TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
: STREET: 1 Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/087,341
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/821,714
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hohenschutz, Liza D.
: REGISTRATION NUMBER: 33,712
: REFERENCE/DOCKET NUMBER: SPNX-0010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 737 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-087-341-2

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Query Match      100.0%; Score 48; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HDAPIGYD 8
Db      85 HDAPIGYD 92

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RESULT 17  
US-08-087-341-4  
Sequence 4, Application US/08087341  
GENERAL INFORMATION:  
APPLICANT: Basta, Patricia V.  
APPLICANT: Burns, David J.  
TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: 1 Liberty Place, 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,341  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/821,714  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: SPNX-0010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 737 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-087-341-4

Query Match 100.0%; Score 48; DB 10; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 18  
US-08-087-341A-2  
Sequence 2, Application US/08087341A  
GENERAL INFORMATION:  
APPLICANT: Basta, Patricia V.  
APPLICANT: Burns, David J.  
TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: 1 Liberty Place, 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,341A

FILING DATE: 02-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/821,714  
FILING DATE: 14-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: SPNX-0317  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 737 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-087-341A-2

Query Match 100.0%; Score 48; DB 10; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
DB 85 HDAPIGYD 92

RESULT 19  
US-08-087-341A-4  
Sequence 4, Application US/08087341A  
GENERAL INFORMATION:  
APPLICANT: Basta, Patricia V.  
APPLICANT: Burns, David J.  
TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: 1 Liberty Place, 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,341A  
FILING DATE: 02-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/821,714  
FILING DATE: 14-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: SPNX-0317  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 737 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-087-341A-4

Query Match 100.0%; Score 48; DB 10; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;



Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 20  
US-09-791-537-27401  
; Sequence 27401, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27401  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-27401

Query Match  
Best Local Similarity 100.0%; Score 48; DB 27; Length 737;  
Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 21  
US-09-791-537-35026  
; Sequence 35026, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35026  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-35026

Query Match  
Best Local Similarity 100.0%; Score 48; DB 27; Length 737;  
Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 22  
US-09-791-537-106216  
; Sequence 106216, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 106216  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-791-537-106216

Query Match  
Best Local Similarity 100.0%; Score 48; DB 27; Length 737;  
Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 23  
US-10-170-205E-13606  
; Sequence 13606, Application US/10170205E  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark  
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN  
; FILE REFERENCE: C1001381  
; CURRENT APPLICATION NUMBER: US/10/170,205E  
; CURRENT FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 40312  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13606  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-205E-13606

Query Match  
Best Local Similarity 100.0%; Score 48; DB 31; Length 737;  
Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 24  
US-10-219-051B-3331  
; Sequence 3331, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT APPLICATION NUMBER: US/10/219,051B  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3331  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156  
; DATABASE ENTRY DATE: 2002-06-15

US-10-219-051B-3331

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
| | | | |  
Db 85 HDAPIGYD 92

RESULT 25

US-10-219-051B-3389  
; Sequence 3389, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3389  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872  
; DATABASE ENTRY DATE: 1999-07-15  
US-10-219-051B-3389

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
| | | | |  
Db 85 HDAPIGYD 92

RESULT 26

US-10-219-051B-3391  
; Sequence 3391, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3391  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156  
; DATABASE ENTRY DATE: 2002-06-15  
US-10-219-051B-3391

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
| | | | |  
Db 85 HDAPIGYD 92

RESULT 27

US-10-219-051B-3393  
; Sequence 3393, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3393  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872  
; DATABASE ENTRY DATE: 1999-07-15  
US-10-219-051B-3393

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
| | | | |  
Db 85 HDAPIGYD 92

RESULT 28

US-10-219-051B-3395  
; Sequence 3395, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3395  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156  
; DATABASE ENTRY DATE: 2002-06-15  
US-10-219-051B-3395

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 29  
US-10-219-051B-3397  
; Sequence 3397, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT APPLICATION NUMBER: US/10/219, 051B  
; PRIOR FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3397  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872  
; DATABASE ENTRY DATE: 1999-07-15  
US-10-219-051B-3397

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 30  
US-10-219-051B-3399  
; Sequence 3399, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT APPLICATION NUMBER: US/10/219, 051B  
; PRIOR FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3399  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156  
; DATABASE ENTRY DATE: 2002-06-15  
US-10-219-051B-3399

Query Match 100.0%; Score 48; DB 32; Length 737;

Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 31  
US-10-219-051B-3401  
; Sequence 3401, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT APPLICATION NUMBER: US/10/219, 051B  
; PRIOR FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3401  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872  
; DATABASE ENTRY DATE: 1999-07-15  
US-10-219-051B-3401

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
|||  
Db 85 HDAPIGYD 92

RESULT 32  
US-10-219-051B-3403  
; Sequence 3403, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT APPLICATION NUMBER: US/10/219, 051B  
; PRIOR FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 3403  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156  
; DATABASE ENTRY DATE: 2002-06-15  
US-10-219-051B-3403

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HDAPIGVD 8  
|||  
Db 85 HDAPIGVD 92

RESULT 33  
US-10-219-051B-4226  
; Sequence 4226, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 4226  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / KIRTC  
; DATABASE ENTRY DATE: 1999-07-15  
US-10-219-051B-4226

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8  
|||  
Db 85 HDAPIGVD 92

RESULT 34  
US-10-219-051B-4228  
; Sequence 4228, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 4228  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156  
; DATABASE ENTRY DATE: 2002-06-15  
US-10-219-051B-4228

Query Match 100.0%; Score 48; DB 32; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8  
|||  
Db 85 HDAPIGVD 92

RESULT 35  
US-10-307-700-24  
; Sequence 24, Application US/10307700  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez-Zulueta, Mirella  
; APPLICANT: Chin, Daniel J.  
; APPLICANT: Wilson, Riche  
; APPLICANT: McFarland, K.C.  
; APPLICANT: Melcher, Thorsten  
; APPLICANT: Wieloch, Tadeusz  
; TITLE OF INVENTION: Ischemia Associated Genes  
; FILE REFERENCE: AGYT-001  
; CURRENT APPLICATION NUMBER: US/10/307,700  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/334,973  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/334,985  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-307-700-24

Query Match 100.0%; Score 48; DB 33; Length 737;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8  
|||  
Db 85 HDAPIGVD 92

RESULT 36  
US-10-466-162-2  
; Sequence 2, Application US/10466162  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling  
; FILE REFERENCE: EX02-001C-PC  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: US/10/466,162  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,335  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,694  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,532  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,361  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,531  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,457  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,226  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,304  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,459  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/261,456  
; PRIOR FILING DATE: 2001-01-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-162-2

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Query Match      100.0%; Score 48; DB 34; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
      |||||
Db      85 HDAPIGYD 92

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RESULT 37
US-10-756-149-4713
; Sequence 4713, Application US/10756149
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4713
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4713

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Query Match      100.0%; Score 48; DB 37; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
      |||||
Db      85 HDAPIGYD 92

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RESULT 38
US-10-932-349-1540
; Sequence 1540, Application US/10932349
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: C0001483
; CURRENT APPLICATION NUMBER: US/10/932,349
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 123188
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1540
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-932-349-1540

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Query Match      100.0%; Score 48; DB 39; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
      |||||
Db      85 HDAPIGYD 92

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RESULT 39
US-11-152-366-28

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; Sequence 28, Application US/11152366
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

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Query Match      100.0%; Score 48; DB 41; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
      |||||
Db      85 HDAPIGYD 92

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RESULT 40
US-60-452-680-12722
; Sequence 12722, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GROPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12722
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-12722

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Query Match      100.0%; Score 48; DB 40; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
      |||||
Db      85 HDAPIGYD 92

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Search completed: December 3, 2005, 23:38:56
Job time : 568 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: December 3, 2005, 23:24:54 ; Search time 6 Seconds  
(without alignments)  
7.450 Million cell updates/sec

Title: US-10-807-553-2  
Perfect score: 48  
Sequence: 1 HDAPICVD 8

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 41035 seqs, 5587842 residues

Total number of hits satisfying chosen parameters: 41035

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Pending Patents AA New:\*  
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2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	8	7	US-11-271-285-1
2	44	91.7	8	7	US-11-271-285-3
3	44	91.7	8	7	US-11-271-285-9
4	43	89.6	8	7	US-11-271-285-4
5	42	87.5	8	7	US-11-271-285-5
6	40	83.3	8	7	US-11-271-285-8
7	40	83.3	8	7	US-11-271-285-10
8	36	75.0	8	7	US-11-271-285-2
9	36	75.0	8	7	US-11-271-285-13
10	35	72.9	8	7	US-11-271-285-6
11	35	72.9	8	7	US-11-271-285-7
12	31	64.6	8	7	US-11-271-285-12
13	29	60.4	261	1	PCT-US05-41373-24
14	29	60.4	261	7	US-11-274-683-24
15	29	60.4	515	8	US-60-732-162-964
16	29	60.4	877	6	US-10-244-081A-33
17	29	60.4	900	6	US-10-244-081A-20
18	28	58.3	136	7	US-11-218-976-19
19	28	58.3	388	7	US-11-218-976-21
20	28	58.3	578	8	US-60-732-162-404
21	28	58.3	683	6	US-10-380-533B-139
22	28	58.3	844	8	US-60-732-162-402
23	28	58.3	899	8	US-60-732-162-408
24	28	58.3	961	8	US-60-732-162-406
25	28	58.3	1199	7	US-11-271-139-2

26	28	58.3	1310	7	US-11-155-906-135	Sequence 135, App
27	28	58.3	1310	7	US-11-154-298-135	Sequence 135, App
28	28	58.3	1337	7	US-11-155-906-134	Sequence 134, App
29	28	58.3	1337	7	US-11-154-298-134	Sequence 134, App
30	28	58.3	1340	7	US-11-155-906-138	Sequence 138, App
31	28	58.3	1340	7	US-11-154-298-138	Sequence 138, App
32	28	58.3	1347	7	US-11-155-906-133	Sequence 133, App
33	28	58.3	1347	7	US-11-154-298-133	Sequence 133, App
34	27	56.2	5	7	US-11-271-285-14	Sequence 14, App
35	27	56.2	33	7	US-11-264-096-783	Sequence 783, App
36	26	54.2	13	7	US-11-152-974A-349	Sequence 349, App
37	26	54.2	13	7	US-11-153-143A-349	Sequence 349, App
38	26	54.2	30	6	US-10-868-184C-3480	Sequence 3480, App
39	26	54.2	168	6	US-10-206-921A-360	Sequence 360, App
40	26	54.2	163	6	US-10-267-849A-10	Sequence 10, App
41	26	54.2	243	8	US-11-265-762-68	Sequence 68, App
42	26	54.2	243	8	US-60-732-162-1654	Sequence 1654, App
43	26	54.2	279	8	US-60-731-733-2	Sequence 2, App
44	26	54.2	290	7	US-11-266-444-3231	Sequence 3231, App
45	26	54.2	290	8	US-60-735-988-3231	Sequence 3231, App
46	26	54.2	309	7	US-11-266-444-3230	Sequence 3230, App
47	26	54.2	309	8	US-60-735-988-3230	Sequence 3230, App
48	26	54.2	455	7	US-11-264-096-1401	Sequence 1401, App
49	26	54.2	481	1	PCT-US05-40306-36	Sequence 36, App
50	26	54.2	481	1	PCT-US05-40255-36	Sequence 36, App
51	26	54.2	481	1	PCT-US05-40256-41	Sequence 41, App
52	26	54.2	481	7	US-11-264-737-41	Sequence 41, App
53	26	54.2	481	7	US-11-265-761-36	Sequence 36, App
54	26	54.2	481	7	US-11-264-784-36	Sequence 36, App
55	26	54.2	678	7	US-11-202-507A-11	Sequence 11, App
56	26	54.2	679	7	US-11-202-507A-5	Sequence 5, App
57	26	54.2	720	6	US-10-206-921A-170	Sequence 170, App
58	26	54.2	1041	7	US-11-283-526-3	Sequence 3, App
59	26	54.2	1574	7	US-11-268-554-114	Sequence 114, App
60	26	54.2	1769	7	US-11-268-554-113	Sequence 113, App
61	26	54.2	2048	7	US-11-268-554-112	Sequence 112, App
62	26	54.2	2048	7	US-11-268-554-117	Sequence 117, App
63	26	54.2	2057	7	US-11-268-554-115	Sequence 115, App
64	26	54.2	2061	7	US-11-268-554-116	Sequence 116, App
65	26	54.2	3385	1	PCT-US05-41273-20	Sequence 20, App
66	26	54.2	3385	7	US-11-274-683-20	Sequence 20, App
67	25	52.1	20	7	US-11-266-444-2900	Sequence 2900, App
68	25	52.1	20	8	US-60-735-988-2900	Sequence 2900, App
69	25	52.1	43	6	US-10-253-471C-1490	Sequence 1490, App
70	25	52.1	55	6	US-10-469-469-193	Sequence 193, App
71	25	52.1	92	6	US-10-868-184C-4210	Sequence 4210, App
72	25	52.1	139	7	US-11-267-310-2	Sequence 2, App
73	25	52.1	139	7	US-11-267-191-2	Sequence 2, App
74	25	52.1	166	6	US-10-868-184C-3174	Sequence 3174, App
75	25	52.1	252	7	US-11-266-444-1416	Sequence 1416, App
76	25	52.1	252	8	US-60-735-988-1416	Sequence 1416, App
77	25	52.1	300	6	US-10-206-921A-18	Sequence 18, App
78	25	52.1	331	7	US-11-264-096-1257	Sequence 1257, App
79	25	52.1	331	7	US-11-197-712-243	Sequence 243, App
80	25	52.1	354	6	US-10-142-638A-70	Sequence 70, App
81	25	52.1	371	7	US-11-274-547-2	Sequence 2, App
82	25	52.1	377	7	US-11-267-310-55	Sequence 55, App
83	25	52.1	377	7	US-11-267-191-55	Sequence 55, App
84	25	52.1	383	7	US-11-267-310-57	Sequence 57, App
85	25	52.1	383	7	US-11-267-191-57	Sequence 57, App
86	25	52.1	391	6	US-10-556-478-2	Sequence 2, App
87	25	52.1	406	8	US-60-732-162-852	Sequence 852, App
88	25	52.1	420	6	US-60-732-162-852	Sequence 852, App
89	25	52.1	432	6	US-10-206-921A-330	Sequence 330, App
90	25	52.1	435	7	US-11-268-554-221	Sequence 221, App
91	25	52.1	437	7	US-11-268-554-220	Sequence 220, App
92	25	52.1	443	6	US-10-997-436-7	Sequence 7, App
93	25	52.1	461	6	US-10-556-478-3	Sequence 3, App
94	25	52.1	471	1	PCT-US05-40306-30	Sequence 30, App
95	25	52.1	471	1	PCT-US05-40255-30	Sequence 30, App
96	25	52.1	471	1	PCT-US05-40256-35	Sequence 35, App
97	25	52.1	471	7	US-11-264-737-35	Sequence 35, App
98	25	52.1	471	7	US-11-265-761-30	Sequence 30, App

99 25 52.1 471 7 US-11-264-784-30 Sequence 30, Appl  
100 25 52.1 503 8 US-60-732-162-850 Sequence 850, App

## ALIGNMENTS

RESULT 1  
US-11-271-285-1  
; Sequence 1, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-11-271-285-1

Query Match 100.0%; Score 48; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 2  
US-11-271-285-3  
; Sequence 3, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-3

Query Match 91.7%; Score 44; DB 7; Length 8;  
Best Local Similarity 87.5%; Pred. No. 3.3e+04;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 3  
US-11-271-285-9

; Sequence 9, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-9

Query Match 91.7%; Score 44; DB 7; Length 8;  
Best Local Similarity 87.5%; Pred. No. 3.3e+04;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 4  
US-11-271-285-4  
; Sequence 4, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-4

Query Match 89.6%; Score 43; DB 7; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3.3e+04;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8  
Db 1 HDAPIGYD 8

RESULT 5  
US-11-271-285-5  
; Sequence 5, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-5



FILE REFERENCE: 58600-8218.US00  
CURRENT APPLICATION NUMBER: US/11/271,285  
CURRENT FILING DATE: 2005-11-10  
PRIOR APPLICATION NUMBER: US 60/626,564  
PRIOR FILING DATE: 2004-11-10  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-5

Query Match 87.5%; Score 42; DB 7; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3.3e+04;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
| | | | |  
Db 1 HDAPLGYE 8

RESULT 6  
US-11-271-285-8  
Sequence 8, Application US/11271285  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Tanaka, Masashi  
APPLICANT: Robbins, Robert C.  
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
FILE REFERENCE: 58600-8218.US00  
CURRENT APPLICATION NUMBER: US/11/271,285  
CURRENT FILING DATE: 2005-11-10  
PRIOR APPLICATION NUMBER: US 60/626,564  
PRIOR FILING DATE: 2004-11-10  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-8

Query Match 83.3%; Score 40; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8  
| | | | |  
Db 2 DAPIGYD 8

RESULT 7  
US-11-271-285-10  
Sequence 10, Application US/11271285  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Tanaka, Masashi  
APPLICANT: Robbins, Robert C.  
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
FILE REFERENCE: 58600-8218.US00  
CURRENT APPLICATION NUMBER: US/11/271,285  
CURRENT FILING DATE: 2005-11-10  
PRIOR APPLICATION NUMBER: US 60/626,564  
PRIOR FILING DATE: 2004-11-10  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn version 3.3

SEQ ID NO 10  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-10

Query Match 83.3%; Score 40; DB 7; Length 8;  
Best Local Similarity 87.5%; Pred. No. 3.3e+04;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
| | | | |  
Db 1 HDAAIGYD 8

RESULT 8  
US-11-271-285-2  
Sequence 2, Application US/11271285  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Tanaka, Masashi  
APPLICANT: Robbins, Robert C.  
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
FILE REFERENCE: 58600-8218.US00  
CURRENT APPLICATION NUMBER: US/11/271,285  
CURRENT FILING DATE: 2005-11-10  
PRIOR APPLICATION NUMBER: US 60/626,564  
PRIOR FILING DATE: 2004-11-10  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-2

Query Match 75.0%; Score 36; DB 7; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3.3e+04;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8  
| | | | |  
Db 1 HEADIGYD 8

RESULT 9  
US-11-271-285-13  
Sequence 13, Application US/11271285  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Tanaka, Masashi  
APPLICANT: Robbins, Robert C.  
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
FILE REFERENCE: 58600-8218.US00  
CURRENT APPLICATION NUMBER: US/11/271,285  
CURRENT FILING DATE: 2005-11-10  
PRIOR APPLICATION NUMBER: US 60/626,564  
PRIOR FILING DATE: 2004-11-10  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 13  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-13

Query Match 75.0%; Score 36; DB 7; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3.3e+04;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIG 8  
Db 1 HDGDI GYD 8

## RESULT 10

US-11-271-285-6  
; Sequence 6, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-6

Query Match 72.9%; Score 35; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6  
Db 1 HDAPIG 6

## RESULT 11

US-11-271-285-7  
; Sequence 7, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-7

Query Match 72.9%; Score 35; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6  
Db 1 HDAPIG 6

Db 1 HDAPIG 6

## RESULT 12

US-11-271-285-12  
; Sequence 12, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; FILE REFERENCE: 58600-8218.US00  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-12

Query Match 64.6%; Score 31; DB 7; Length 8;  
Best Local Similarity 83.3%; Pred. No. 3.3e+04;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6  
Db 1 HDAPIG 6

## RESULT 13

PCT-US05-41273-24  
; Sequence 24, Application PC/TUS0541273  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Haltli, Bradley A  
; TITLE OF INVENTION: Blatophyllin biosynthetic gene cluster  
; FILE REFERENCE: 1855/257  
; CURRENT APPLICATION NUMBER: PCT/US05/41273  
; CURRENT FILING DATE: 2005-11-23  
; PRIOR APPLICATION NUMBER: US 60/627,752  
; PRIOR FILING DATE: 2004-11-12  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Streptomyces sp. NRRL 30748  
PCT-US05-41273-24

Query Match 60.4%; Score 29; DB 1; Length 261;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 5  
Db 64 HDAPIG 68

## RESULT 14

US-11-274-683-24  
; Sequence 24, Application US/11274683  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Haltli, Bradley A  
; TITLE OF INVENTION: Blatophyllin biosynthetic gene cluster  
; FILE REFERENCE: 1855/256

;; CURRENT APPLICATION NUMBER: US/11/274,683  
;; CURRENT FILING DATE: 2005-11-14  
;; PRIOR APPLICATION NUMBER: US 60/627,752  
;; PRIOR FILING DATE: 2004-11-12  
;; NUMBER OF SEQ ID NOS: 55  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 24  
;; LENGTH: 261  
;; TYPE: PRT  
;; ORGANISM: Streptomyces sp. NRRL 30748  
US-11-274-683-24

Query Match 60.4%; Score 29; DB 7; Length 261;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPI 5  
Db 64 HDAPI 68

RESULT 15  
US-60-732-162-964  
;; Sequence 964, Application US/60732162  
;; GENERAL INFORMATION:  
;; APPLICANT: Belouchi, Abdelmajid  
;; APPLICANT: Raelson, John V  
;; APPLICANT: Bradley, Walter E  
;; APPLICANT: Paquin, Bruno  
;; APPLICANT: Fournier, Helene  
;; APPLICANT: Nguyen-Huu, Quynh  
;; APPLICANT: Croteau, Pascal  
;; APPLICANT: Allard, Rene  
;; APPLICANT: Debrus, Sophie  
;; APPLICANT: Berdewegh, Paul V  
;; APPLICANT: Little, Randall D  
;; APPLICANT: Keith, Tim  
;; APPLICANT: Segal, Jonathan  
;; TITLE OF INVENTION: Genemap of the Human Genes Associated with Asthma Disease  
;; FILE REFERENCE: 059908-5010-PR  
;; CURRENT APPLICATION NUMBER: US/60/732,162  
;; CURRENT FILING DATE: 2005-11-02  
;; NUMBER OF SEQ ID NOS: 4417  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 964  
;; LENGTH: 515  
;; TYPE: PRT  
;; ORGANISM: Homosapiens  
US-60-732-162-964

Query Match 60.4%; Score 29; DB 8; Length 515;  
Best Local Similarity 83.3%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGY 7  
Db 129 DAPIGY 134

RESULT 16  
US-10-244-081A-33  
;; Sequence 33, Application US/10244081A  
;; GENERAL INFORMATION:  
;; APPLICANT: Lee, Jun  
;; APPLICANT: Gerard, Gary  
;; APPLICANT: Shandilya, Harini  
;; APPLICANT: Griffiths, Katherine Rachel  
;; APPLICANT: Gibbs, Moreland David  
;; APPLICANT: Leonard, Peter  
;; APPLICANT: Bergquist, Peter Leonard  
;; APPLICANT: Potter, Jason  
;; TITLE OF INVENTION: DNA Polymerases and Mutants Thereof  
;; FILE REFERENCE: 0942,5360001

;; CURRENT APPLICATION NUMBER: US/10/244,081A  
;; CURRENT FILING DATE: 2002-09-16  
;; PRIOR APPLICATION NUMBER: US 60/318,903  
;; PRIOR FILING DATE: 2001-09-14  
;; NUMBER OF SEQ ID NOS: 3641  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 33  
;; LENGTH: 877  
;; TYPE: PRT  
;; ORGANISM: Bacillus caldolenax  
US-10-244-081A-33

Query Match 60.4%; Score 29; DB 6; Length 877;  
Best Local Similarity 100.0%; Pred. No. 1,3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPI 5  
Db 328 HDAPI 332

RESULT 17  
US-10-244-081A-20  
;; Sequence 20, Application US/10244081A  
;; GENERAL INFORMATION:  
;; APPLICANT: Lee, Jun  
;; APPLICANT: Gerard, Gary  
;; APPLICANT: Shandilya, Harini  
;; APPLICANT: Griffiths, Katherine Rachel  
;; APPLICANT: Gibbs, Moreland David  
;; APPLICANT: Leonard, Peter  
;; APPLICANT: Bergquist, Peter Leonard  
;; APPLICANT: Potter, Jason  
;; TITLE OF INVENTION: DNA Polymerases and Mutants Thereof  
;; FILE REFERENCE: 0942,5360001  
;; CURRENT APPLICATION NUMBER: US/10/244,081A  
;; CURRENT FILING DATE: 2002-09-16  
;; PRIOR APPLICATION NUMBER: US 60/318,903  
;; PRIOR FILING DATE: 2001-09-14  
;; NUMBER OF SEQ ID NOS: 3641  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 20  
;; LENGTH: 900  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Bacillus caldolyticus EAI DNA polymerase  
US-10-244-081A-20

Query Match 60.4%; Score 29; DB 6; Length 900;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPI 5  
Db 352 HDAPI 356

RESULT 18  
US-11-218-976-19  
;; Sequence 19, Application US/11218976  
;; GENERAL INFORMATION:  
;; APPLICANT: Bertozzi, Carolyn  
;; APPLICANT: Williams, Spencer J.  
;; APPLICANT: Mougous, Joseph  
;; TITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins  
;; FILE REFERENCE: BERK-012DIV2  
;; CURRENT APPLICATION NUMBER: US/11/218,976  
;; CURRENT FILING DATE: 2005-09-01  
;; PRIOR APPLICATION NUMBER: 10/286,606  
;; PRIOR FILING DATE: 2002-10-31  
;; PRIOR APPLICATION NUMBER: 10/891,383

; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 60/285,394  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/345,953  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 10/126,279  
; PRIOR FILING DATE: 2002-04-19  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Mycobacterium bovis  
US-11-218-976-19

Query Match 58.3%; Score 28; DB 7; Length 136;  
Best Local Similarity 50.0%; Pred. No. 29;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HDAPGYD 8  
DB 28 HTGPTGYE 35

RESULT 19  
US-11-218-976-21  
; Sequence 21, Application US/11218976  
; GENERAL INFORMATION:  
; APPLICANT: Bertozzi, Carolyn  
; APPLICANT: Williams, Spencer J.  
; APPLICANT: Mougous, Joseph  
; TITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins  
; FILE REFERENCE: BERK-012DIV2  
; CURRENT APPLICATION NUMBER: US/11/218,976  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: 10/286,606  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 10/891,383  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 60/285,394  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/345,953  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 10/126,279  
; PRIOR FILING DATE: 2002-04-19  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-11-218-976-21

Query Match 58.3%; Score 28; DB 7; Length 388;  
Best Local Similarity 50.0%; Pred. No. 88;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HDAPGYD 8  
DB 106 HTGPTGYE 113

RESULT 20  
US-60-732-162-404  
; Sequence 404, Application US/60732162  
; GENERAL INFORMATION:  
; APPLICANT: Belouchi, Abdelmajid  
; APPLICANT: Raelson, John V  
; APPLICANT: Bradley, Walter E  
; APPLICANT: Paquin, Bruno  
; APPLICANT: Fournier, Helene  
; APPLICANT: Nguyen-Huu, Quynh

; APPLICANT: Croteau, Pascal  
; APPLICANT: Allard, Rene  
; APPLICANT: Debrus, Sophie  
; APPLICANT: Berdewesh, Paul V  
; APPLICANT: Little, Randall D  
; APPLICANT: Keith, Tim  
; APPLICANT: Segal, Jonathan  
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease  
; FILE REFERENCE: 059908-5010-PR  
; CURRENT APPLICATION NUMBER: US/60/732,162  
; CURRENT FILING DATE: 2005-11-02  
; NUMBER OF SEQ ID NOS: 4417  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 404  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-60-732-162-404

Query Match 58.3%; Score 28; DB 8; Length 578;  
Best Local Similarity 57.1%; Pred. No. 1,3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPGYD 8  
DB 466 EAPLAYD 472

RESULT 21  
US-10-380-533B-139  
; Sequence 139, Application US/10380533B  
; GENERAL INFORMATION:  
; APPLICANT: University College Cardiff Consultants Ltd  
; TITLE OF INVENTION: Transglutaminase Gene Products  
; FILE REFERENCE: P504074PCT  
; CURRENT APPLICATION NUMBER: US/10/380,533B  
; CURRENT FILING DATE: 2003-09-30  
; PRIOR APPLICATION NUMBER: GB0111995.7  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: GB0022768.6  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 144  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 139  
; LENGTH: 683  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-380-533B-139

Query Match 58.3%; Score 28; DB 6; Length 683;  
Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 DAPGYD 8  
DB 337 DLPKGYD 343

RESULT 22  
US-60-732-162-402  
; Sequence 402, Application US/60732162  
; GENERAL INFORMATION:  
; APPLICANT: Belouchi, Abdelmajid  
; APPLICANT: Raelson, John V  
; APPLICANT: Bradley, Walter E  
; APPLICANT: Paquin, Bruno  
; APPLICANT: Fournier, Helene  
; APPLICANT: Nguyen-Huu, Quynh  
; APPLICANT: Croteau, Pascal  
; APPLICANT: Allard, Rene  
; APPLICANT: Debrus, Sophie  
; APPLICANT: Berdewesh, Paul V  
; APPLICANT: Little, Randall D

```
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 402
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-402
```

```
Query Match      58.3%; Score 28; DB 8; Length 844;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
Db      349 EAPLAYD 355
```

```
RESULT 23
US-60-732-162-408
; Sequence 408, Application US/60732162
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Debrus, Sophie
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Little, Randall D
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 408
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-408
```

```
Query Match      58.3%; Score 28; DB 8; Length 899;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
Db      404 EAPLAYD 410
```

```
RESULT 24
US-60-732-162-406
; Sequence 406, Application US/60732162
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
```

```
; APPLICANT: Debrus, Sophie
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Little, Randall D
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 406
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-406
```

```
Query Match      58.3%; Score 28; DB 8; Length 961;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
Db      466 EAPLAYD 472
```

```
RESULT 25
US-11-271-139-2
; Sequence 2, Application US/11271139
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTOR 1
; FILE REFERENCE: R-801
; CURRENT APPLICATION NUMBER: US/11/271,139
; PRIOR FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/10/179,408
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/301,061
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1199
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-271-139-2
```

```
Query Match      58.3%; Score 28; DB 7; Length 1199;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 APIGYD 8
Db      755 APVCYN 760
```

```
RESULT 26
US-11-155-906-135
; Sequence 135, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Bld, Pia M.
; APPLICANT: Paris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; CURRENT FILING DATE: 2005-06-17
```

```

; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 1310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-906-135

Query Match          58.3%; Score 28; DB 7; Length 1310;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HDAPIGY 7
        |||
        1046 HGLPLGY 1052

Db      1046 HGLPLGY 1052

RESULT 27
US-11-154-298-135
; Sequence 135, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Ge, Mangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 1310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-298-135

Query Match          58.3%; Score 28; DB 7; Length 1310;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HDAPIGY 7
        |||
        1046 HGLPLGY 1052

Db      1046 HGLPLGY 1052

RESULT 28
US-11-155-906-134
; Sequence 134, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/155,906
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-298-134

Query Match          58.3%; Score 28; DB 7; Length 1337;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HDAPIGY 7
        |||
        1073 HGLPLGY 1079

Db      1073 HGLPLGY 1079
```

```

; APPLICANT: Ge, Mangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-906-134

Query Match          58.3%; Score 28; DB 7; Length 1337;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HDAPIGY 7
        |||
        1073 HGLPLGY 1079

Db      1073 HGLPLGY 1079

RESULT 29
US-11-154-298-134
; Sequence 134, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Farris, Mary
; APPLICANT: Ge, Mangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-298-134

Query Match          58.3%; Score 28; DB 7; Length 1337;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HDAPIGY 7
        |||
        1073 HGLPLGY 1079

Db      1073 HGLPLGY 1079
```

```
RESULT 30
US-11-155-906-138
; Sequence 138, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 1340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-906-138
```

```
Query Match          58.3%; Score 28; DB 7; Length 1340;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 HDAPIGY 7
DB 1078 HGLPLGY 1084
```

```
RESULT 31
US-11-154-298-138
; Sequence 138, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 1340
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-11-154-298-138
```

```
Query Match          58.3%; Score 28; DB 7; Length 1340;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 HDAPIGY 7
DB 1078 HGLPLGY 1084
```

```
RESULT 32
US-11-155-906-133
; Sequence 133, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 1347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-906-133
```

```
Query Match          58.3%; Score 28; DB 7; Length 1347;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 HDAPIGY 7
DB 1083 HGLPLGY 1089
```

```
RESULT 33
US-11-154-298-133
; Sequence 133, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
```

; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US60/286,630  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 708  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 133  
; LENGTH: 1347  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-154-298-133

Query Match 58.3%; Score 28; DB 7; Length 1347;  
Best Local Similarity 57.1%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIGY 7  
DB 1083 HGLPELY 1089

RESULT 34  
US-11-271-285-14  
; Sequence 14, Application US/11271285  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Tanaka, Masashi  
; APPLICANT: Robbins, Robert C.  
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted  
; TITLE OF INVENTION: Organ  
; FILE REFERENCE: 58600-8218, US800  
; CURRENT APPLICATION NUMBER: US/11/271,285  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 60/626,564  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Patencin version 3.3  
; SEQ ID NO 14  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-271-285-14

Query Match 56.2%; Score 27; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIG 6  
DB 1 DAPIG 5

RESULT 35  
US-11-264-096-783  
; Sequence 783, Application US/11264096  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PFS46D1  
; CURRENT APPLICATION NUMBER: US/11/264,096  
; CURRENT FILING DATE: 2005-11-02  
; PRIOR APPLICATION NUMBER: 09/833,245  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229,358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256,931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199,384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 783

; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-264-096-783

Query Match 56.2%; Score 27; DB 7; Length 33;  
Best Local Similarity 66.7%; Pred. No. 10;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIG 6  
DB 21 HPAVIG 26

RESULT 36  
US-11-152-974A-349  
; Sequence 349, Application US/11152974A  
; GENERAL INFORMATION:  
; APPLICANT: Wayne F. Beyer, Jr.  
; APPLICANT: Robin Hyde-Deruysscher  
; APPLICANT: Paul T. Hamilton  
; APPLICANT: Ray Edward Benson  
; TITLE OF INVENTION: IPMs to Promote the Specific Attachment of Target Analytes to the  
; TITLE OF INVENTION: of Orthopedic Implants  
; FILE REFERENCE: AFP006  
; CURRENT APPLICATION NUMBER: US/11/152,974A  
; CURRENT FILING DATE: 2005-06-15  
; PRIOR APPLICATION NUMBER: 60/580,019  
; PRIOR FILING DATE: 2004-06-16  
; PRIOR APPLICATION NUMBER: 60/651,338  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/651,747  
; PRIOR FILING DATE: 2005-02-10  
; NUMBER OF SEQ ID NOS: 558  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 349  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Isolated from phage display libraries  
US-11-152-974A-349

Query Match 54.2%; Score 26; DB 7; Length 13;  
Best Local Similarity 66.7%; Pred. No. 5.9;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 APIGYD 8  
DB 8 SPAGYD 13

RESULT 37  
US-11-153-143A-349  
; Sequence 349, Application US/11153143A  
; GENERAL INFORMATION:  
; APPLICANT: Paul T. Hamilton  
; APPLICANT: Mark W. Grinstaff  
; APPLICANT: Daniel J. Kenan  
; APPLICANT: Dale J. Christensen  
; TITLE OF INVENTION: Biofunctional Coatings  
; FILE REFERENCE: AFP005  
; CURRENT APPLICATION NUMBER: US/11/153,143A  
; CURRENT FILING DATE: 2005-06-15  
; PRIOR APPLICATION NUMBER: 60/580,019  
; PRIOR FILING DATE: 2004-06-16  
; PRIOR APPLICATION NUMBER: 60/651,338  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/651,747  
; PRIOR FILING DATE: 2005-02-10  
; NUMBER OF SEQ ID NOS: 558  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 349



```
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: isolated from phage display libraries
US-11-153-143A-349

Query Match          54.2%; Score 26; DB 7; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 APGYD 8
      : |||
Db      8 SPAGYD 13

RESULT 38
US-10-868-184C-3480
/ Sequence 3480, Application US/10868184C
/ GENERAL INFORMATION:
/ APPLICANT: Rosen, et. al
/ TITLE OF INVENTION: Human Secreted Proteins
/ FILE REFERENCE: P8605
/ CURRENT APPLICATION NUMBER: US/10/868,184C
/ CURRENT FILING DATE: 2004-06-16
/ PRIOR APPLICATION NUMBER: 60/278,650
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 09/833,245
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: PCT/US01/11988
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: PCT/US00/06043
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: PCT/US00/06012
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: PCT/US00/06058
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: PCT/US00/06044
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: PCT/US00/06059
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: PCT/US00/06042
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: PCT/US00/06014
/ PRIOR FILING DATE: 2000-03-09
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 13046
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3480
/ LENGTH: 30
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-868-184C-3480

Query Match          54.2%; Score 26; DB 6; Length 30;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPGY 7
      : |||
Db      20 HELPGY 26

RESULT 39
US-10-206-921A-360
/ Sequence 360, Application US/10206921A
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
```

```
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zhenli
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: 39780-3430R1C515
/ CURRENT APPLICATION NUMBER: US/10/206,921A
/ CURRENT FILING DATE: 2002-07-26
/ PRIOR APPLICATION NUMBER: US 10/052,586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: US 60/232,887
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 360
/ LENGTH: 148
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-206-921A-360

Query Match          54.2%; Score 26; DB 6; Length 148;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 HDAPGYD 8
      : |||
Db      139 HGASVNYD 146

RESULT 40
US-10-267-849A-10
/ Sequence 10, Application US/10267849A
/ GENERAL INFORMATION:
/ APPLICANT: Ji et al.
/ TITLE OF INVENTION: Breast Specific Genes and Proteins
/ FILE REFERENCE: P158C1
/ CURRENT APPLICATION NUMBER: US/10/267,849A
/ CURRENT FILING DATE: 2002-10-10
/ PRIOR APPLICATION NUMBER: US 08/673,284
/ PRIOR FILING DATE: 1996-06-28
/ PRIOR APPLICATION NUMBER: US 60/000,602
/ PRIOR FILING DATE: 1995-06-30
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 10
/ LENGTH: 163
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (14)..(14)
/ OTHER INFORMATION: The 'Xaa' at location 14 stands for Lys, Asn, Arg, Ser, Thr, Ile,
/ OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
/ OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (36)..(36)
/ OTHER INFORMATION: The 'Xaa' at location 36 stands for Lys, Glu, Gln, or a stop
/ OTHER INFORMATION: codon.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (40)..(40)
/ OTHER INFORMATION: The 'Xaa' at location 40 stands for Lys, Asn, Arg, Ser, Thr, Ile,
/ OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
/ OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (70)..(70)
/ OTHER INFORMATION: The 'Xaa' at location 70 stands for Arg, or Ser.
/ FEATURE:
```

NAME/KEY: misc\_feature  
 LOCATION: (71)..(71)  
 OTHER INFORMATION: The 'Xaa' at location 71 stands for Glu, Gly, Ala, or Val.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (72)..(72)  
 OTHER INFORMATION: The 'Xaa' at location 72 stands for Glu, Gly, Ala, or Val.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (103)..(103)  
 OTHER INFORMATION: The 'Xaa' at location 103 stands for Lys, Asn, Arg, Ser, Thr,  
 OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop  
 OTHER INFORMATION: codon, Tyr, Trp, Cys, or Phe.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (105)..(105)  
 OTHER INFORMATION: The 'Xaa' at location 105 stands for Asn, Asp, His, or Tyr.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (108)..(108)  
 OTHER INFORMATION: The 'Xaa' at location 108 stands for Ieu, or Phe.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (116)..(116)  
 OTHER INFORMATION: The 'Xaa' at location 116 stands for Asn, Ser, Thr, or Ile.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (118)..(118)  
 OTHER INFORMATION: The 'Xaa' at location 118 stands for a stop codon, Ser, or Ieu.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (124)..(124)  
 OTHER INFORMATION: The 'Xaa' at location 124 stands for Arg, Gly, or Trp.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (125)..(125)  
 OTHER INFORMATION: The 'Xaa' at location 125 stands for Ile, Val, Ieu, or Phe.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (130)..(130)  
 OTHER INFORMATION: The 'Xaa' at location 130 stands for Arg, or Ser.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (135)..(135)  
 OTHER INFORMATION: The 'Xaa' at location 135 stands for Asp, Gly, Ala, or Val.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (137)..(137)  
 OTHER INFORMATION: The 'Xaa' at location 137 stands for Tyr, Cys, Ser, or Phe.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (142)..(142)  
 OTHER INFORMATION: The 'Xaa' at location 142 stands for Thr, Ala, Pro, or Ser.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (147)..(147)  
 OTHER INFORMATION: The 'Xaa' at location 147 stands for Ieu, or Phe.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (155)..(155)  
 OTHER INFORMATION: The 'Xaa' at location 155 stands for Asn, Ser, Thr, or Ile.  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (159)..(159)  
 OTHER INFORMATION: The 'Xaa' at location 159 stands for Lys, Arg, Thr, or Met.  
 NAME/KEY: misc\_feature  
 LOCATION: (160)..(160)  
 OTHER INFORMATION: The 'Xaa' at location 160 stands for Lys, Glu, Gln, or a  
 OTHER INFORMATION: stop codon.  
 US-10-267-849A-10

Query Match

54.2%, Score 26, DB 6, Length 163,

Best Local Similarity 66.7%; Pred. No. 88;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 DAPGY 7  
 Db 1 DSPAGY 6

Search completed: December 3, 2005, 23:29:23  
 Job time : 7 secs